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(54) Titre : ANTIGENES DE STREPTOCOQUE
(54) Title: STREPTOCOCCUS ANTIGENS

(57) Abrégé/Abstract:

Streptococcus polypeptides and polynucleotides encoding them are disclosed. Said polypeptides may be useful vaccine components for the prophylaxis or therapy of streptococcus infection in animals. Also disclosed are recombinant methods of producing the protein antigens as well as diagnostic assays for detecting streptococcus bacterial infection.

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WO 01/098334 A3

(54) Title: **STREPTOCOCCUS ANTIGENS**

(57) Abstract: Streptococcus polypeptides and polynucleotides encoding them are disclosed. Said polypeptides may be useful vaccine components for the prophylaxis or therapy of streptococcus infection in animals. Also disclosed are recombinant methods of producing the protein antigens as well as diagnostic assays for detecting streptococcus bacterial infection.

STREPTOCOCCUS ANTIGENSFIELD OF THE INVENTION

The present invention is related to antigens, epitopes and
5 antibodies directed to these epitopes, more particularly
polypeptide antigens of streptococcus pneumoniae pathogen
which may be useful for prophylaxis, diagnostic or treatment
of streptococcal infection.

10

BACKGROUND OF THE INVENTION

S. pneumoniae is an important agent of disease in man
especially among infants, the elderly and immunocompromised
persons. It is a bacterium frequently isolated from patients
15 with invasive diseases such as bacteraemia/septicaemia,
pneumonia, meningitis with high morbidity and mortality
throughout the world. Even with appropriate antibiotic
therapy, pneumococcal infections still result in many deaths.
Although the advent of antimicrobial drugs has reduced the
20 overall mortality from pneumococcal disease, the presence of
resistant pneumococcal organisms has become a major problem in
the world today. Effective pneumococcal vaccines could have a
major impact on the morbidity and mortality associated with S.
pneumoniae disease. Such vaccines would also potentially be
25 useful to prevent otitis media in infants and young children.

Efforts to develop a pneumococcal vaccine have generally
concentrated on generating immune responses to the pneumococcal
capsular polysaccharide. More than 80 pneumococcal capsular
30 serotypes have been identified on the basis of antigenic
differences. The currently available pneumococcal vaccine,
comprising 23 capsular polysaccharides that most frequently
caused disease, has significant shortcomings related primarily
to the poor immunogenicity of some capsular polysaccharides,
35 the diversity of the serotypes and the differences in the
distribution of serotypes over time, geographic areas and age

groups. In particular, the failure of existing vaccines and capsular conjugate vaccines currently in development to protect young children against all serotypes spurs evaluation of other S. pneumoniae components. Although immunogenicity of capsular polysaccharides can be improved, serotype specificity will still represent a major limitation of polysaccharide-based vaccines. The use of a antigenically conserved immunogenic pneumococcal protein antigen, either by itself or in combination with additional components, offers the possibility of a protein-based pneumococcal vaccine.

PCT WO 98/18930 published May 7, 1998 entitled "*Streptococcus Pneumoniae* antigens and vaccines" describes certain polypeptides which are claimed to be antigenic. However, no biological activity of these polypeptides is reported. Similarly, no sequence conservation is reported, which is a necessary species common vaccine candidate.

PCT WO 00/39299 describes polypeptides and polynucleotides encoding these polypeptides. PCT WO 00/39299 demonstrates that polypeptides designated as BVH-3 and BVH-11 provide protection against fatal experimental infection with pneumococci.

Therefore there remains an unmet need for *Streptococcus* antigens that may be used as components for the prophylaxis, diagnostic and/or therapy of *Streptococcus* infection.

30 SUMMARY OF THE INVENTION

An isolated polynucleotide comprising a polynucleotide chosen from;

35

- (a) a polynucleotide encoding a polypeptide having at least 70% identity to a second polypeptide chosen from: table A, B, D, E or H;

- (b) a polynucleotide encoding a polypeptide having at least 95% identity to a second polypeptide chosen from: table A, B, D, E or H;
- 5 (c) a polynucleotide encoding a polypeptide having an amino sequence chosen from table A, B, D, E or H; or fragments, analogs or derivatives thereof;
- (d) a polynucleotide encoding a polypeptide chosen from: table A, B, D, E or H;
- 10 (e) a polynucleotide encoding a polypeptide capable of generating antibodies having binding specificity for a polypeptide having a sequence chosen from: table A, B, D, E or H;
- (f) a polynucleotide encoding an epitope bearing portion of a polypeptide chosen from table A, B, D, E or H; and
- 15 (g) a polynucleotide complementary to a polynucleotide in (a), (b), (c), (d), (e) or (f).

In other aspects, there are provided novel polypeptides encoded by polynucleotides of the invention, pharmaceutical or vaccine composition, vectors comprising polynucleotides of the invention operably linked to an expression control region, as well as host cells transfected with said vectors and methods of producing polypeptides comprising culturing said host cells under conditions suitable for expression.

25

BRIEF DESCRIPTION OF THE DRAWINGS

Figure 1 is the DNA sequence of SP64 BVH-3 gene; SEQ ID NO: 1

30 Figure 2 is a DNA sequence containing the complete SP64 BVH-3 gene at nucleotides 1777 to 4896; SEQ ID NO: 2

Figure 3 is the DNA sequence of SP64 BVH-11 gene; SEQ ID NO: 3

35 Figure 4 is a DNA sequence containing the complete SP64 BVH-11 gene at nucleotides 45 to 2567; SEQ ID NO: 4

Figure 5 is a DNA sequence containing the complete SP64 BVH-11-2 gene at nucleotides 114 to 2630; SEQ ID NO: 5

5 Figure 6 is the amino acid sequence of SP64 BVH-3 polypeptide; SEQ ID NO: 6

Figure 7 is the amino acid sequence of SP64 BVH-11 polypeptide; SEQ ID NO: 7

10

Figure 8 is the amino acid sequence of SP64 BVH-11-2 polypeptide; SEQ ID NO: 8

Figure 9 is the DNA sequence of SP63 BVH-3 gene; SEQ ID NO: 9

15

Figure 10 is the amino acid sequence of SP63 BVH-3 polypeptide; SEQ ID NO: 10

Figure 11 is the amino acid sequence of 4D4.9 polypeptide; SEQ ID NO: 11

20

Figure 12 is the amino acid sequence of 7G11.7 polypeptide; SEQ ID NO: 12

25 Figure 13 is the amino acid sequence of 7G11.9 polypeptide; SEQ ID NO: 13

Figure 14 is the amino acid sequence of 4D3.4 polypeptide; SEQ ID NO: 14

30

Figure 15 is the amino acid sequence of 8E3.1 polypeptide; SEQ ID NO: 15

Figure 16 is the amino acid sequence of 1G2.2 polypeptide; SEQ ID NO: 16

35

Figure 17 is the amino acid sequence of 10C12.7 polypeptide;
SEQ ID NO: 17

Figure 18 is the amino acid sequence of 14F6.3 polypeptide;
5 SEQ ID NO: 18

Figure 19 is the amino acid sequence of B12D8.2 polypeptide;
SEQ ID NO: 19

10 Figure 20 is the amino acid sequence of 7F4.1 polypeptide; SEQ
ID NO: 20

Figure 21 is the amino acid sequence of 10D7.5 polypeptide;
SEQ ID NO: 21
15

Figure 22 is the amino acid sequence of 10G9.3 polypeptide,
10A2.2 polypeptide and B11B8.1 polypeptide; SEQ ID NO: 22

Figure 23 is the amino acid sequence of 11B8.4 polypeptide;
20 SEQ ID NO: 23

Figure 24 is the amino acid sequence of Mab H11B-11B8 target
epitope; SEQ ID 163

25 Figure 25 is a schematic representation of the BVH-3 gene as
well as location of gene sequences coding for the full length
and truncated polypeptides. The relationships between DNA
fragments are shown with respect to each other.

30 Figure 26 is a schematic representation of the BVH-11 gene as
well as location of gene sequences coding for the full length
and truncated polypeptides. The relationships between DNA
fragments are shown with respect to each other.

35 Figure 27 is a schematic representation of the BVH-11-2 gene
as well as location of gene sequences coding for the full

length and truncated polypeptides. The relationships between DNA fragments are shown with respect to each other.

Figure 28 is a schematic representation of the BVH-3 protein and the location of internal and surface epitopes recognized by certain monoclonal antibodies.

Figure 29 is a schematic representation of the BVH-11-2 protein and the location of protective surface epitopes recognized by certain monoclonal antibodies.

Figure 30 is a map of plasmid pURV22.HIS. Kan^R, kanamycin-resistance coding region; cI857, bacteriophage λ cI857 temperature-sensitive repressor gene; lambda pL, bacteriophage λ transcription promoter; His-tag, 6-histidine coding region; terminator, T1 transcription terminator; ori, colE1 origin of replication.

Figure 31 depicts the comparison of the amino acid sequences of BVH-3M (sp64) and BVH-3 (Sp63) proteins by using the program Clustal W from MacVector sequence analysis software (version 6.5.3). Underneath the alignment, there is a consensus line where * and . characters indicate identical and similar amino acid residues, respectively.

Figure 32 depicts the comparison of the amino acid sequences of BVH-3, BVH-11 and BVH-11-2 proteins by using the program Clustal W from MacVector sequence analysis software (version 6.5.3). Underneath the alignment, there is a consensus line where * and . characters indicate identical and similar amino acid residues, respectively.

Figure 33 is the DNA sequence of the NEW43 gene (SEQ ID No 257).

Figure 34 is the deduced amino acid sequence of NEW43 polypeptide (SEQ ID No 258).

5 DETAILED DESCRIPTION OF THE INVENTION

It was determined that portions of the BVH-3 and BVH-11 polypeptides were internal. Other portions were not present in important strains such as encapsulated s.pneumonia causing
10 disease strains. It would be advantageous to have a polypeptide that comprises a portion that is not internal. When large portions of a polypeptide are internal, these portions are not exposed on the bacteria. However, these portions can be very immunogenic in a recombinant polypeptide
15 and will not confer protection against infections. It would also be advantageous to have a polypeptide that comprises a portion that is present in most strains.

The present invention is concerned with polypeptides in which
20 undesired portions have been deleted and/or modified in order to obtain a specific immune response.

In accordance with the present invention, there are also provided polypeptides or polynucleotides encoding such
25 polypeptides comprising protective domains.

Surprisingly, when the undesired portion of the polypeptides are deleted or modified, the polypeptides have desired biological properties. This is surprising in view of the fact
30 that some of these portions were described as being epitope bearing portion in the patent application PCT WO 98/18930. In other publications such as PCT WO 00/37105, portions identified as histidine triad and coil coiled regions were said to be of importance. The present inventors have found that variants of
35 the polypeptide BVH-3 and BVH-11 in which certain portions were deleted and/or modified and chimeras of these polypeptides have

biological properties and generate a specific immune response.

According to one aspect, the present invention provides an isolated polynucleotide encoding a polypeptide having at least
5 70% identity to a second polypeptide comprising a sequence as disclosed in the present application, the tables and figures.

In accordance with one aspect of the present invention, there is provided an isolated polynucleotide comprising a
10 polynucleotide chosen from;

- (a) a polynucleotide encoding a polypeptide having at least 70% identity to a second polypeptide chosen from: table B, E or H;
- 15 (b) a polynucleotide encoding a polypeptide having at least 95% identity to a second polypeptide chosen from: table B, E or H;
- (c) a polynucleotide encoding a polypeptide having an amino sequence chosen from table B, E or H or fragments, analogs or derivatives thereof;
- 20 (d) a polynucleotide encoding a polypeptide chosen from: table B, E or H;
- (e) a polynucleotide encoding a polypeptide capable of generating antibodies having binding specificity for a polypeptide having a sequence chosen from: table B, E or
25 H,
- (f) a polynucleotide encoding an epitope bearing portion of a polypeptide chosen from table B, E or H; and
- (g) a polynucleotide complementary to a polynucleotide in
30 (a), (b), (c), (d), (e) or (f).

According to one aspect, the present invention provides an isolated polynucleotide encoding a polypeptide having at least
70% identity to a second polypeptide comprising a sequence
35 chosen from table A, B, D, E, G or H or fragments, analogues or derivatives thereof.

According to one aspect, the present invention provides an isolated polynucleotide encoding a polypeptide having at least 95% identity to a second polypeptide comprising a sequence
5 chosen from table A, B, D, E, G or H or fragments, analogues or derivatives thereof.

According to one aspect, the present invention relates to polypeptides characterised by the amino acid sequence chosen
10 from table A, B, D, E, G or H or fragments, analogues or derivatives thereof.

According to one aspect, the present invention provides an isolated polynucleotide encoding a polypeptide having at least
15 70% identity to a second polypeptide comprising a sequence chosen from table A, B, D, E, G or H.

According to one aspect, the present invention provides an isolated polynucleotide encoding a polypeptide having at least
20 95% identity to a second polypeptide comprising a sequence chosen from table A, B, D, E, G or H.

According to one aspect, the present invention relates to polypeptides characterised by the amino acid sequence chosen
25 from table A, B, D, E, G or H.

According to one aspect, the present invention provides an isolated polynucleotide encoding a polypeptide having at least 70% identity to a second polypeptide comprising a sequence
30 chosen from table B, E or H or fragments, analogues or derivatives thereof.

According to one aspect, the present invention provides an isolated polynucleotide encoding a polypeptide having at least
35 95% identity to a second polypeptide comprising a sequence chosen from B, E or H or fragments, analogues or derivatives

thereof.

According to one aspect, the present invention relates to polypeptides characterised by the amino acid sequence chosen
5 from table B, E or H or fragments, analogues or derivatives thereof.

According to one aspect, the present invention provides an isolated polynucleotide encoding a polypeptide having at least
10 70% identity to a second polypeptide comprising a sequence chosen from table B, E or H.

According to one aspect, the present invention provides an isolated polynucleotide encoding a polypeptide having at least
15 95% identity to a second polypeptide comprising a sequence chosen from B, E or H.

According to one aspect, the present invention relates to polypeptides characterised by the amino acid sequence chosen
20 from table B, E or H.

In accordance with the present invention, all nucleotides encoding polypeptides and chimeric polypeptides are within the scope of the present invention.

25

In a further embodiment, the polypeptides or chimeric polypeptides in accordance with the present invention are antigenic.

30 In a further embodiment, the polypeptides or chimeric polypeptides in accordance with the present invention are immunogenic.

In a further embodiment, the polypeptides or chimeric
35 polypeptides in accordance with the present invention can elicit an immune response in an individual.

In a further embodiment, the present invention also relates to polypeptides which are able to raise antibodies having binding specificity to the polypeptides or chimeric polypeptides of the present invention as defined above.

10 In one embodiment, the polypeptides of table A (BVH-3) or table D (BVH-11) comprise at least one epitope bearing portion.

In a further embodiment, the fragments of the polypeptides of the present invention will comprise one or more epitope bearing portion identified in Table C and F. The fragment will comprises at least 15 contiguous amino acid of the polypeptide of table C and F. The fragment will comprises at least 20 contiguous amino acid of the polypeptide of table C and F.

20 In a further embodiment, the epitope bearing portion of the polypeptide of table A(BVH-3) comprises at least one polypeptide listed in Table C.

In a further embodiment, the epitope bearing portion of the polypeptide of table B(BVH-11) comprises at least one polypeptide listed in Table F.

25 An antibody that " has binding specificity" is an antibody that recognises and binds the selected polypeptide but which does not substantially recognise and bind other molecules in a sample, such as a biological sample. Specific binding can be measured using an ELISA assay in which the selected polypeptide is used as an antigen.

35 Unless otherwise defined, all technical and scientific terms used herein have the same meaning as commonly understood by one of ordinary skill in the art to which this invention belongs. All publications, patent applications, patents, and

other references mentioned herein are incorporated by reference in their entirety. In case of conflict, the present specification, including definitions, will control. In addition, the materials, methods, and examples are
5 illustrative only and not intended to be limiting.

In accordance with the present invention, "protection" in the biological studies is defined by a significant increase in the survival curve, rate or period. Statistical analysis using the
10 Log rank test to compare survival curves, and Fisher exact test to compare survival rates and numbers of days to death, respectively, might be useful to calculate P values and determine whether the difference between the two groups is statistically significant. P values of 0.05 are regarded as
15 not significant.

As used herein, "fragments", "derivatives" or "analogues" of the polypeptides of the invention include those polypeptides in which one or more of the amino acid residues are
20 substituted with a conserved or non-conserved amino acid residue (preferably conserved) and which may be natural or unnatural. In one embodiment, derivatives and analogues of polypeptides of the invention will have about 70% identity with those sequences illustrated in the figures or fragments
25 thereof. That is, 70% of the residues are the same. In a further embodiment, polypeptides will have greater than 75% homology. In a further embodiment, polypeptides will have greater than 80% homology. In a further embodiment, polypeptides will have greater than 85% homology. In a further
30 embodiment, polypeptides will have greater than 90% homology. In a further embodiment, polypeptides will have greater than 95% homology. In a further embodiment, polypeptides will have greater than 99% homology. In a further embodiment, derivatives and analogues of polypeptides of the invention
35 will have less than about 20 amino acid residue substitutions, modifications or deletions and more preferably less than 10.

Preferred substitutions are those known in the art as conserved i.e. the substituted residues share physical or chemical properties such as hydrophobicity, size, charge or functional groups.

5

The skilled person will appreciate that analogues or derivatives of the proteins or polypeptides of the invention will also find use in the context of the present invention, i.e. as antigenic/immunogenic material. Thus, for instance
10 proteins or polypeptides which include one or more additions, deletions, substitutions or the like are encompassed by the present invention. In addition, it may be possible to replace one amino acid with another of similar "type". For instance replacing one hydrophobic amino acid with another hydrophilic
15 amino acid.

One can use a program such as the CLUSTAL program to compare amino acid sequences. This program compares amino acid sequences and finds the optimal alignment by inserting spaces
20 in either sequence as appropriate. It is possible to calculate amino acid identity or similarity (identity plus conservation of amino acid type) for an optimal alignment. A program like BLASTx will align the longest stretch of similar sequences and assign a value to the fit. It is thus possible
25 to obtain a comparison where several regions of similarity are found, each having a different score. Both types of identity analysis are contemplated in the present invention.

In an alternative approach, the analogues or derivatives could
30 be fusion proteins, incorporating moieties which render purification easier, for example by effectively tagging the desired protein or polypeptide. It may be necessary to remove the "tag" or it may be the case that the fusion protein itself retains sufficient antigenicity to be useful.

35

In an additional aspect of the invention there are provided antigenic/immunogenic fragments of the proteins or polypeptides of the invention, or of analogues or derivatives thereof.

5

The fragments of the present invention should include one or more such epitopic regions or be sufficiently similar to such regions to retain their antigenic/immunogenic properties. Thus, for fragments according to the present invention the degree of identity is perhaps irrelevant, since they may be 100% identical to a particular part of a protein or polypeptide, analogue or derivative as described herein. The key issue, once again, is that the fragment retains the antigenic/immunogenic properties.

15

Thus, what is important for analogues, derivatives and fragments is that they possess at least a degree of the antigenicity/immunogenic of the protein or polypeptide from which they are derived.

20

In accordance with the present invention, polypeptides of the invention include both polypeptides and chimeric polypeptides.

25

Also included are polypeptides which have fused thereto other compounds which alter the polypeptides biological or pharmacological properties i.e. polyethylene glycol (PEG) to increase half-life; leader or secretory amino acid sequences for ease of purification; prepro- and pro- sequences; and (poly)saccharides.

30

Furthermore, in those situations where amino acid regions are found to be polymorphic, it may be desirable to vary one or more particular amino acids to more effectively mimic the different epitopes of the different streptococcus strains.

35

Moreover, the polypeptides of the present invention can be

modified by terminal $-NH_2$ acylation (e.g. by acetylation, or thioglycolic acid amidation, terminal carboxy amidation, e.g. with ammonia or methylamine) to provide stability, increased hydrophobicity for linking or binding to a support or other molecule.

Also contemplated are hetero and homo polypeptide multimers of the polypeptide fragments, analogues and derivatives. These polymeric forms include, for example, one or more polypeptides that have been cross-linked with cross-linkers such as avidin/biotin, gluteraldehyde or dimethylsuperimide. Such polymeric forms also include polypeptides containing two or more tandem or inverted contiguous sequences, produced from multicistronic mRNAs generated by recombinant DNA technology.

Preferably, a fragment, analogue or derivative of a polypeptide of the invention will comprise at least one antigenic region i.e. at least one epitope.

In order to achieve the formation of antigenic polymers (i.e. synthetic multimers), polypeptides may be utilised having bishaloacetyl groups, nitroarylhalides, or the like, where the reagents being specific for thio groups. Therefore, the link between two mercapto groups of the different peptides may be a single bond or may be composed of a linking group of at least two, typically at least four, and not more than 16, but usually not more than about 14 carbon atoms.

In a particular embodiment, polypeptide fragments, analogues and derivatives of the invention do not contain a methionine (Met) starting residue. Preferably, polypeptides will not incorporate a leader or secretory sequence (signal sequence). The signal portion of a polypeptide of the invention may be determined according to established molecular biological techniques. In general, the polypeptide of interest may be isolated from a streptococcus culture and subsequently

sequenced to determine the initial residue of the mature protein and therefore the sequence of the mature polypeptide.

According to another aspect, there are provided vaccine
5 compositions comprising one or more streptococcus polypeptides of the invention in admixture with a pharmaceutically acceptable carrier diluent or adjuvant. Suitable adjuvants include oils i.e. Freund's complete or incomplete adjuvant; salts i.e. $AlK(SO_4)_2$, $AlNa(SO_4)_2$, $AlNH_4(SO_4)_2$, silica, kaolin,
10 carbon polynucleotides i.e. poly IC and poly AU. Preferred adjuvants include QuilA and Alhydrogel. Vaccines of the invention may be administered parenterally by injection, rapid infusion, nasopharyngeal absorption, dermoabsorption, or bucal or oral. Pharmaceutically acceptable carriers also include
15 tetanus toxoid.

The term vaccine is also meant to include antibodies. In accordance with the present invention, there is also provided the use of one or more antibodies having binding specificity
20 for the polypeptides of the present invention for the treatment or prophylaxis of streptococcus infection and/or diseases and symptoms mediated by streptococcus infection.

Vaccine compositions of the invention are used for the
25 treatment or prophylaxis of streptococcus infection and/or diseases and symptoms mediated by streptococcus infection as described in P.R. Murray (Ed, in chief), E.J. Baron, M.A. Pfaller, F.C. Tenover and R.H. Yolken. Manual of Clinical Microbiology, ASM Press, Washington, D.C. sixth edition, 1995,
30 1482p which are herein incorporated by reference. In one embodiment, vaccine compositions of the present invention are used for the treatment or prophylaxis of meningitis, otitis media, bacteremia or pneumonia. In one embodiment, vaccine compositions of the invention are used for the treatment or
35 prophylaxis of streptococcus infection and/or diseases and symptoms mediated by streptococcus infection, in particular

S.pneumoniae, group A streptococcus (pyogenes), group B streptococcus (GBS or agalactiae), dysgalactiae, uberis, nocardia as well as Staphylococcus aureus. In a further embodiment, the streptococcus infection is S.pneumoniae.

5

In a particular embodiment, vaccines are administered to those individuals at risk of streptococcus infection such as infants, elderly and immunocompromised individuals.

- 10 As used in the present application, the term " individuals" include mammals. In a further embodiment, the mammal is human.

Vaccine compositions are preferably in unit dosage form of about 0.001 to 100 µg/kg (antigen/body weight) and more preferably 0.01 to 10 µg/kg and most preferably 0.1 to 1 µg/kg 1 to 3 times with an interval of about 1 to 6 week intervals between immunizations.

20 Vaccine compositions are preferably in unit dosage form of about 0.1 µg to 10 mg and more preferably 1µg to 1 mg and most preferably 10 to 100 µg 1 to 3 times with an interval of about 1 to 6 week intervals between immunizations.

25 According to another aspect, there are provided polynucleotides encoding polypeptides characterised by the amino acid sequence chosen from table A, B, D, E, G or H or fragments, analogues or derivatives thereof.

30 According to another aspect, there are provided polynucleotides encoding polypeptides characterised by the amino acid sequence chosen from table B, E or H or fragments, analogues or derivatives thereof.

35 In one embodiment, polynucleotides are those illustrated in table A, B, D, E, G or H which encodes polypeptides of the

invention.

In one embodiment, polynucleotides are those illustrated in table B, E or H which encodes polypeptides of the invention.

5 It will be appreciated that the polynucleotide sequences illustrated in the figures may be altered with degenerate codons yet still encode the polypeptides of the invention. Accordingly the present invention further provides
10 polynucleotides which hybridise to the polynucleotide sequences herein above described (or the complement sequences thereof) having 50% identity between sequences. In one embodiment, at least 70% identity between sequences. In one embodiment, at least 75% identity between sequences. In one
15 embodiment, at least 80% identity between sequences. In one embodiment, at least 85% identity between sequences. In one embodiment, at least 90% identity between sequences. In a further embodiment, polynucleotides are hybridizable under stringent conditions i.e. having at least 95% identity. In a
20 further embodiment, more than 97% identity.

Suitable stringent conditions for hybridation can be readily determined by one of skilled in the art (see for example Sambrook et al., (1989) Molecular cloning : A Laboratory
25 Manual, 2nd ed, Cold Spring Harbor, N.Y.; Current Protocols in Molecular Biology, (1999) Edited by Ausubel F.M. et al., John Wiley & Sons, Inc., N.Y.).

In a further embodiment, the present invention provides
30 polynucleotides that hybridise under stringent conditions to either

- (a) a DNA sequence encoding a polypeptide or
- (b) the complement of a DNA sequence encoding a polypeptide;

35 wherein said polypeptide comprising a sequence chosen from table A, B, D, E, G or H or fragments or analogues thereof.

In a further embodiment, the present invention provides polynucleotides that hybridise under stringent conditions to
5 either

(c) a DNA sequence encoding a polypeptide or

(d) the complement of a DNA sequence encoding a polypeptide;

wherein said polypeptide comprising a sequence chosen from
10 table B, E or H or fragments or analogues thereof.

In a further embodiment, the present invention provides polynucleotides that hybridise under stringent conditions to either

15 (a) a DNA sequence encoding a polypeptide or

(b) the complement of a DNA sequence encoding a polypeptide;

wherein said polypeptide comprises at least 10 contiguous amino acid residues from a polypeptide comprising a sequence chosen
20 from table A, B, D, E, G or H or fragments or analogues thereof.

In a further embodiment, the present invention provides polynucleotides that hybridise under stringent conditions to
25 either

(c) a DNA sequence encoding a polypeptide or

(d) the complement of a DNA sequence encoding a polypeptide;

wherein said polypeptide comprises at least 10 contiguous amino
30 acid residues from a polypeptide comprising a sequence chosen from table B, E or H or fragments or analogues thereof.

In a further embodiment, polynucleotides are those encoding polypeptides of the invention illustrated in table A, B, D, E,
35 G or H.

As will be readily appreciated by one skilled in the art, polynucleotides include both DNA and RNA.

The present invention also includes polynucleotides
5 complementary to the polynucleotides described in the present application.

In a further aspect, polynucleotides encoding polypeptides of the invention, or fragments, analogues or derivatives thereof,
10 may be used in a DNA immunization method. That is, they can be incorporated into a vector which is replicable and expressible upon injection thereby producing the antigenic polypeptide in vivo. For example polynucleotides may be incorporated into a plasmid vector under the control of the
15 CMV promoter which is functional in eukaryotic cells. Preferably the vector is injected intramuscularly.

According to another aspect, there is provided a process for producing polypeptides of the invention by recombinant
20 techniques by expressing a polynucleotide encoding said polypeptide in a host cell and recovering the expressed polypeptide product. Alternatively, the polypeptides can be produced according to established synthetic chemical techniques i.e. solution phase or solid phase synthesis of
25 oligopeptides which are ligated to produce the full polypeptide (block ligation).

General methods for obtention and evaluation of polynucleotides and polypeptides are described in the
30 following references: Sambrook et al, Molecular Cloning: A Laboratory Manual, 2nd ed, Cold Spring Harbor, N.Y., 1989; Current Protocols in Molecular Biology, Edited by Ausubel F.M. et al., John Wiley and Sons, Inc. New York; PCR Cloning Protocols, from Molecular Cloning to Genetic Engineering,
35 Edited by White B.A., Humana Press, Totowa, New Jersey, 1997, 490 pages; Protein Purification, Principles and Practices,

Scopes R.K., Springer-Verlag, New York, 3rd Edition, 1993, 380 pages; Current Protocols in Immunology, Edited by Coligan J.E. et al., John Wiley & Sons Inc., New York which are herein incorporated by reference.

5

For recombinant production, host cells are transfected with vectors which encode the polypeptide, and then cultured in a nutrient media modified as appropriate for activating promoters, selecting transformants or amplifying the genes.

10 Suitable vectors are those that are viable and replicable in the chosen host and include chromosomal, non-chromosomal and synthetic DNA sequences e.g. bacterial plasmids, phage DNA, baculovirus, yeast plasmids, vectors derived from combinations of plasmids and phage DNA. The polypeptide sequence may be
15 incorporated in the vector at the appropriate site using restriction enzymes such that it is operably linked to an expression control region comprising a promoter, ribosome binding site (consensus region or Shine-Dalgarno sequence), and optionally an operator (control element). One can select
20 individual components of the expression control region that are appropriate for a given host and vector according to established molecular biology principles (Sambrook et al, Molecular Cloning: A Laboratory Manual, 2nd ed, Cold Spring Harbor, N.Y., 1989; Current Protocols in Molecular Biology, Edited by Ausubel F.M. et al., John Wiley and Sons, Inc. New
25 York incorporated herein by reference). Suitable promoters include but are not limited to LTR or SV40 promoter, E.coli lac, tac or trp promoters and the phage lambda P_L promoter. Vectors will preferably incorporate an origin of replication
30 as well as selection markers i.e. ampicilin resistance gene. Suitable bacterial vectors include pET, pQE70, pQE60, pQE-9, pbs, pD10 phagescript, psiX174, pbluescript SK, pbsks, pNH8A, pNH16a, pNH18A, pNH46A, ptrc99a, pKK223-3, pKK233-3, pDR540, pRIT5 and eukaryotic vectors pBlueBacIII, pWLNEO, pSV2CAT,
35 pOG44, pXT1, pSG, pSVK3, pBPV, pMSG and pSVL. Host cells may be bacterial i.e. E.coli, Bacillus subtilis, Streptomyces;

fungal i.e. Aspergillus niger, Aspergillus nidulans; yeast i.e. Saccharomyces or eukaryotic i.e. CHO, COS.

Upon expression of the polypeptide in culture, cells are typically harvested by centrifugation then disrupted by physical or chemical means (if the expressed polypeptide is not secreted into the media) and the resulting crude extract retained to isolate the polypeptide of interest. Purification of the polypeptide from culture media or lysate may be achieved by established techniques depending on the properties of the polypeptide i.e. using ammonium sulfate or ethanol precipitation, acid extraction, anion or cation exchange chromatography, phosphocellulose chromatography, hydrophobic interaction chromatography, hydroxylapatite chromatography and lectin chromatography. Final purification may be achieved using HPLC.

The polypeptide may be expressed with or without a leader or secretion sequence. In the former case the leader may be removed using post-translational processing (see US 4,431,739; US 4,425,437; and US 4,338,397 incorporated herein by reference) or be chemically removed subsequent to purifying the expressed polypeptide.

According to a further aspect, the streptococcus polypeptides of the invention may be used in a diagnostic test for streptococcus infection, in particular S. pneumoniae infection. Several diagnostic methods are possible, for example detecting streptococcus organism in a biological sample, the following procedure may be followed:

- a) obtaining a biological sample from a patient;
- b) incubating an antibody or fragment thereof reactive with a streptococcus polypeptide of the invention with the biological sample to form a mixture; and
- c) detecting specifically bound antibody or bound fragment in the mixture which indicates the presence of streptococcus.

Alternatively, a method for the detection of antibody specific to a streptococcus antigen in a biological sample containing or suspected of containing said antibody may be performed as follows:

- a) obtaining a biological sample from a patient;
- b) incubating one or more streptococcus polypeptides of the invention or fragments thereof with the biological sample to form a mixture; and
- 10 c) detecting specifically bound antigen or bound fragment in the mixture which indicates the presence of antibody specific to streptococcus.

One of skill in the art will recognize that this diagnostic test may take several forms, including an immunological test such as an enzyme-linked immunosorbent assay (ELISA), a radioimmunoassay or a latex agglutination assay, essentially to determine whether antibodies specific for the polypeptide are present in an organism.

20

The DNA sequences encoding polypeptides of the invention may also be used to design DNA probes for use in detecting the presence of streptococcus in a biological sample suspected of containing such bacteria. The detection method of this invention comprises:

- a) obtaining the biological sample from a patient;
- b) incubating one or more DNA probes having a DNA sequence encoding a polypeptide of the invention or fragments thereof with the biological sample to form a mixture; and
- 30 c) detecting specifically bound DNA probe in the mixture which indicates the presence of streptococcus bacteria.

The DNA probes of this invention may also be used for detecting circulating streptococcus i.e. S.pneumoniae nucleic acids in a sample, for example using a polymerase chain reaction, as a method of diagnosing streptococcus infections.

35

The probe may be synthesized using conventional techniques and may be immobilized on a solid phase, or may be labelled with a detectable label. A preferred DNA probe for this application is an oligomer having a sequence complementary to at least
5 about 6 contiguous nucleotides of the streptococcus pneumoniae polypeptides of the invention.

Another diagnostic method for the detection of streptococcus in a patient comprises:

- 10 a) labelling an antibody reactive with a polypeptide of the invention or fragment thereof with a detectable label;
- b) administering the labelled antibody or labelled fragment to the patient; and
- c) detecting specifically bound labelled antibody or labelled
15 fragment in the patient which indicates the presence of streptococcus.

A further aspect of the invention is the use of the streptococcus polypeptides of the invention as immunogens for
20 the production of specific antibodies for the diagnosis and in particular the treatment of streptococcus infection. Suitable antibodies may be determined using appropriate screening methods, for example by measuring the ability of a particular antibody to passively protect against streptococcus infection
25 in a test model. One example of an animal model is the mouse model described in the examples herein. The antibody may be a whole antibody or an antigen-binding fragment thereof and may belong to any immunoglobulin class. The antibody or fragment may be of animal origin, specifically of mammalian origin and
30 more specifically of murine, rat or human origin. It may be a natural antibody or a fragment thereof, or if desired, a recombinant antibody or antibody fragment. The term recombinant antibody or antibody fragment means antibody or antibody fragment which was produced using molecular biology
35 techniques. The antibody or antibody fragments may be polyclonal, or preferably monoclonal. It may be specific for

a number of epitopes associated with the streptococcus pneumoniae polypeptides but is preferably specific for one.

A further aspect of the invention is the use of the antibodies
 5 directed to the streptococcus polypeptides of the invention for passive immunization. One could use the antibodies described in the present application. Suitable antibodies may be determined using appropriate screening methods, for example by measuring the ability of a particular antibody to passively
 10 protect against streptococcus infection in a test model. One example of an animal model is the mouse model described in the examples herein. The antibody may be a whole antibody or an antigen-binding fragment thereof and may belong to any immunoglobulin class. The antibody or fragment may be of
 15 animal origin, specifically of mammalian origin and more specifically of murine, rat or human origin. It may be a natural antibody or a fragment thereof, or if desired, a recombinant antibody or antibody fragment. The term recombinant antibody or antibody fragment means antibody or
 20 antibody fragment which was produced using molecular biology techniques. The antibody or antibody fragments may be polyclonal, or preferably monoclonal. It may be specific for a number of epitopes associated with the streptococcus pneumoniae polypeptides but is preferably specific for one.

25 The following are reference tables summarizing the sequences disclosed in the present application:

TABLE A, B and C Variants and Epitope of BVH-3-

30

Table A

Family	Polypeptide SEQ ID NO
BVH-3	
New 21	aa 396-1039 of SEQ ID. 6
New 25	aa 233-1039 of SEQ ID.6
New 40	aa 408-1039 of SEQ ID.6

TABLE B -

Family	Polypeptide SEQ ID NO
BVH-3	
NEW1-mut1**	235
NEW35A	236
NEW42	237
NEW49	238
NEW50	239
NEW51	240
NEW52	241
NEW53	242
NEW54	243
NEW55	244
NEW56	245
NEW56-mut2**	245
NEW56-mut3**	245
NEW57	246
NEW63	247
NEW64	248
NEW65	249
NEW66	250
NEW76	251
NEW105	252
NEW106	253
NEW107	254

- 5 ** silent mutation, i.e. the polypeptide is the same as New1 or New 56

TABLE C- Epitopes of BVH-3

7G11.7	12
7G11.9	13
B12D8.2	19
7F4.1	20
14F6.3	18
4D3.4	14
10C12.7	17
8E3.1	15
1G2.2	16

TABLE D, E and F Variants and Epitope of BVH-11-5 TABLE D-

Family	Polypeptide SEQ ID NO
BVH-11	
New19	aa 497-838 of Seq.ID 8
New24	aa 227-838 of Seq.ID 8

TABLE E-

Family	Polypeptide SEQ ID NO
BVH-11	
New 43	258
NEW60	293
NEW61	294
NEW62	295
NEW80	296
NEW81	297
NEW82	298
NEW83	299
NEW84	300
NEW85	301
NEW88D1	302
NEW88D2	303
NEW88	304

10

TABLE F- epitopes of BVH-11

10D7.5	21
10G9.3	22
B11B8.1	22
10A2.2	22
11b8.4	23
3A4.1	24

15

TABLE G and H Chimeras-TABLE G

Family	Polypeptide SEQ ID NO
--------	-----------------------

Chimeras with BVH-11 and BVH-3	
New17	M*-NEW5-G*P*-NEW1
New20	M*-NEW1-G*P*-NEW5
New26	M*-NEW10-G*P*-NEW25
New27	M*-NEW19-G*P*-NEW25
New28	M*-NEW10-G*P*-NEW1
New29	M*-NEW5-G*P*-NEW25
New30	M*-NEW4-G*P*-NEW25
New31	M*-NEW4-G*P*-NEW1
NEW32	M*-NE19-G*P*-NEW1

* OPTIONAL AMINO ACID

TABLE H

Family	Polypeptide SEQ ID NO.
Chimeras with BVH-11 and BVH-3	
VP 89	305
VP 90	306
VP 91	307
VP 92	308
VP 93	309
VP 94	310
VP 108	311
VP109	312
VP 110	313
VP 111	314
VP112	315
VP113	316
VP114	317
VP115	318
VP116	319
VP117	320
VP119	321
VP120	322
VP121	323
VP122	324
VP123	325
VP124	326

5

EXAMPLE 1

This example describes the bacterial strains, plasmids, PCR
primers, recombinant proteins and hybridoma antibodies used
10 herein.

S. pneumoniae SP64 (serogroup 6) and SP63 (serogroup 9) clinical isolates were provided by the Laboratoire de la Santé Publique du Québec, Sainte-Anne-de-Bellevue; Rx1 strain, a nonencapsulated derivative of the type 2 strain D39 and the
5 type 3 strain WU2 were provided by David E. Briles from University of Alabama, Birmingham and the type 3 clinical isolate P4241 was provided by the Centre de Recherche en Infectiologie du Centre Hospitalier de l'Université Laval, Sainte-Foy. E. coli strains DH5 α (Gibco BRL, Gaithersburg,
10 MD); AD494 (λ DE3) (Novagen, Madison, WI) and BL21 (λ DE3) (Novagen) as well as plasmid superlinker pSL301 vector (Invitrogen, San Diego, CA); pCMV-GH vector (gift from Dr. Stephen A. Johnston, Department for Biochemistry, University of Texas, Dallas, Texas); pET32 and pET21 (Novagen) and
15 pURV22.HIS expression vectors (Figure 30) were used in this study. The pURV22.HIS vector contains a cassette of the bacteriophage λ cI857 temperature-sensitive repressor gene from which the functional P_R promoter has been deleted. The inactivation of the cI857 repressor by a temperature increase
20 from the range of 30-37°C to 37-42°C results in the induction of the gene under the control of promoter λ PL. The PCR primers used for the generation of the recombinant plasmids had a restriction endonuclease site at the 5'end, thereby allowing directional cloning of the amplified product into the
25 digested plasmid vector. The PCR oligonucleotide primers used are listed in the following Table 1. The location of the gene sequences coding for BVH-3, BVH-11 and BVH-11-2 gene products is summarized in the Figure 25, Figure 26 and Figure 27, respectively.

30

Table 1. List of PCR oligonucleotide primers

Primer	SEQ ID NO	Sequence 5' - 3'	Nucleotide position	Restriction sites
OCRR 479	25	cagtagatctgtgcctatgcact aaac	SEQ ID 1: 61-78 SEQ ID 9: 1-18	BglII
OCRR 480	26	gatctctagactactgctattcc ttacgctatg	SEQ ID 2: 4909-4887 SEQ ID 9: 2528-2519	XbaI
OCRR 497	27	atcactcgagcattacctggata atcctgt	SEQ ID 1: 1525-1506	XhoI
OCRR 498	28	ctgctaagcttatgaaagattta gat	SEQ ID 1: 1534-1548	HindIII
OCRR 499	29	gatactcgagctgctattcctta c	SEQ ID 2: 4906-4893	XhoI
HAMJ 172	30	gaatctcgagttaagctgctgct aattc	SEQ ID 1: 675-661	XhoI
HAMJ 247	31	gacgctcgagcgctatgaaatca gataaattc	SEQ ID 1: 3117-3096	XhoI
HAMJ 248	32	gacgctcgagggcattacctgga taatcctgttcattg	SEQ ID 1: 1527-1501	XhoI
HAMJ 249	33	cagtagatctcttcatcatttat tgaaaagagg	SEQ ID 2: 1749-1771	BglII
HAMJ 278	34	ttattttcttccatatggacttga cagaagagcaaattaag	SEQ ID 1: 1414-1437	NdeI
HAMJ 279	35	cgccaagcttcgctatgaaatca gataaattc	SEQ ID 1: 3117-3096	HindIII
HAMJ 280	36	cgccaagcttttccacaataataa gtcgattgatt	SEQ ID 1: 2400-2377	HindIII
HAMJ 281	37	ttattttcttccatatggaagtac ctatcttggaagaa	SEQ ID 1: 2398-2421	NdeI
HAMJ 300	38	ttattttcttccatatggtgccta tgcactaaaccagc	SEQ ID 1: 62-82	NdeI

Primer	SEQ ID NO	Sequence 5' - 3'	Nucleotide position	Restriction sites
HAMJ 313	39	ataagaatgcggccgcttccaca atataagtcgattgatt	SEQ ID 1: 2400-2377	NotI
OCRR 487	40	cagtagatctgtgcttatgaact aggtttgc	SEQ ID 3: 58-79	BglII
OCRR 488	41	gatcaagcttgctgctaccttta cttactctc	SEQ ID 4: 2577-2556	HindIII
HAMJ 171	42	ctgagatatccggttatcgttcaa acc	SEQ ID 3: 1060-1075	EcoRV
HAMJ 251	43	ctgcaagcttttaaggggaata atacg	SEQ ID 3: 1059-1045	HindIII
HAMJ 264	44	cagtagatctgcagaagccttcc tatctg	SEQ ID 3: 682-700	BglII
HAMJ 282	45	tcgccaagcttcggttatcgttca aaccattggg	SEQ ID 3: 1060-1081	HindIII
HAMJ 283	46	ataagaatgcggccgccttactc tcctttaataaagccaatagtt	SEQ ID 3: 2520-2492	NotI
HAMJ 284	47	catgccatggacattgatagtct cttgaaacagc	SEQ ID 3: 856-880	NcoI
HAMJ 285	48	cgccaagcttcttactctccttt aataaagccaatag	SEQ ID 3: 2520-2494	HindIII
HAMJ 286	49	cgacaagcttaacatggctcgcta gcgttacc	SEQ ID 3: 2139-2119 SEQ ID 5: 2210-2190	HindIII
HAMJ 287	50	cataccatgggcctttatgaggc acctaag	SEQ ID 3: 2014-2034	NcoI
HAMJ 288	51	cgacaagcttaagtaaattcttca gcctctctcag	SEQ ID 3: 2376-2353	HindIII
HAMJ 289	52	gataccatggctagcgacatgt tcaaagaa	SEQ ID 3: 2125-2146	NcoI
HAMJ 290	53	cgccaagcttatcatccactaac ttgactttatcac	SEQ ID 3: 1533-1508	HindIII

Primer	SEQ ID NO	Sequence 5' - 3'	Nucleotide position	Restriction sites
HAMJ 291	54	cataccatggatattcttgccctt cttagctccg	SEQ ID 3: 1531-1554	NcoI
HAMJ 301	55	catgccatggtgcttatgaacta ggtttgc	SEQ ID 3: 59-79	NcoI
HAMJ 302	56	cgccaagcttttagcggttacaaa accattatc	SEQ ID 3: 2128-2107	HindIII
HAMJ 160	57	gtattagatctgttcctatgaac ttggtcgtcacca	SEQ ID 5: 172-196	BglII
HAMJ 186	58	cgcctctagactactgtatagga gccgg	SEQ ID 5: 2613-2630	XbaI
HAMJ 292	59	catgccatggaaaacatttcaag ccttttacgtg	SEQ ID 5: 925-948	NcoI
HAMJ 293	60	cgacaagcttctgtataggagcc ggttgactttc	SEQ ID 5: 2627-2604	HindIII
HAMJ 294	61	catgccatggttcgtaaaaataa ggcagaccaag	SEQ ID 5: 2209-2232	NcoI
HAMJ 297	62	catgccatggaagcctattggaa tggaag	SEQ ID 5: 793-812	NcoI
HAMJ 352	63	catgccatggaagcctattggaa tggaagc	SEQ ID 5: 793-813	NcoI
HAMJ 353	64	cgccaagcttgtaggtaatttgc gcatttgg	SEQ ID 5: 1673-1653	HindIII
HAMJ 354	65	cgccaagcttctgtataggagcc ggttgac	SEQ ID 5: 2627-2608	HindIII
HAMJ 355	66	catgccatggatattcttgccctt cttagctcc	SEQ ID 5: 1603-1624	NcoI
HAMJ 404	67	ttatttcttccatatgcatggtg atcatttccattaca	SEQ ID 1: 1186-1207	NdeI
HAMJ 464	68	gatgcatatgaatatgcaaccga gtcagttaagc	SEQ ID 1: 697-720	NdeI
HAMJ 465	69	gatgctcgagagcatcaaateccg tatccatc	SEQ ID 1: 1338-1318	XhoI

Primer	SEQ ID NO	Sequence 5' - 3'	Nucleotide position	Restriction sites
HAMJ 466	70	gatgcatatggatcatttccatt acattcca	SEQ ID 1: 1192-1212	NdeI
HAMJ 467	71	gacaagcttggcattacctggat aatcctg	SEQ ID 1: 1527-1507	HindIII
HAMJ 352	72	catgccatggaagcctattggaa tggaagc	SEQ ID 5: 793-813	NcoI
HAMJ 470	73	ataagaatgcggccgcccgtatg aaatcagataaatc	SEQ ID 1: 3096-3117	NotI
HAMJ 471	168	atatggggccctgtataggagcc ggttgacttcc	SEQ ID 5: 2626-2604	Apa I
HAMJ 472	169	atatggggcccaatatgcaaccga gtcagttaagc	SEQ ID 1: 720-697	Apa I
HAMJ 350	170	atatggggcccaacatggctcgcta gcgttacc	SEQ ID 3: 2139-2119	Apa I
HAMJ 351	171	tcccggggcccgacttgacagaag agcaaattaag	SEQ ID 1: 1414-1437	Apa I
HAMJ 358	172	catgccatgggacttgacagaag agcaaattaag	SEQ ID 1: 1415-1437	NcoI
HAMJ 359	173	tcccggggcccgctatgaaatca gataaatc	SEQ ID 1: 3116-3096	Apa I
HAMJ 403	174	atatggggcccgacattgatagtc tcttgaaacagc	SEQ ID 3: 856-880	Apa I
HAMJ 361	175	cgccaagcttaacatggctcgcta gcgttacc	SEQ ID 3: 2139-2119	Hind III
HAMJ 483	176	atatggggcccttactctccttt aataaagccaatag	SEQ ID 3: 2520-2494	Apa I

Molecular biology techniques were performed according to standard methods. See for example, Sambrook, J., Fritsch, E.F., Maniatis, T., "Molecular cloning. A laboratory manual" Vol.1-2-3 (second edition) Cold Spring Harbour Laboratory Press, 1989, New York, which is herein incorporated by reference. PCR-amplified products were digested with restriction endonucleases and ligated to either linearized plasmid pSL301, pCMV-GH, pET or pURV22.HIS expression vector digested likewise or digested with enzymes that produce compatible cohesive ends. Recombinant pSL301 and recombinant pCMV-GH plasmids were digested with restriction enzymes for the in-frame cloning in pET expression vector. When pET

vectors were used, clones were first stabilized in *E. coli* DH5 α before introduction into *E. coli* BL21(Δ DE3) or AD494 (Δ DE3) for expression of full-length or truncated BVH-3, BVH-11 or BVH-11-2 molecules. Each of the resultant plasmid constructs was confirmed by nucleotide sequence analysis. The recombinant proteins were expressed as N-terminal fusions with the thioredoxin and His-tag (pET32 expression system); as C-terminal fusions with an His-tag (pET21 expression system); or as N-terminal fusions with an His-tag (pURV22.HIS expression system). The expressed recombinant proteins were purified from supernatant fractions obtained after centrifugation of sonicated IPTG- (pET systems) or heat- (pURV22.HIS) induced *E. coli* using a His-Bind metal chelation resin (QIAGEN, Chatsworth, CA). The gene products generated from *S. pneumoniae* SP64 are listed in the following Table 2. The gene fragment encoding BVH-3-Sp63 protein (amino acid residues 21 to 840 on SEQ ID NO: 10) was generated from *S. pneumoniae* SP63 using the PCR-primer sets OCRR479-OCRR480 and the cloning vector pSL301. The recombinant pSL301-BVH-3Sp63 was digested for the in-frame cloning in pET32 vector for the expression of the BVH-3-Sp63 molecule.

Table 2. Lists of truncated BVH-3, BVH-11, BVH-11-2 and Chimeric gene products generated from *S. pneumoniae* SP64

PCR-primer sets	Protein designation	Identification	Encoded amino acids (SEQ ID No6)	Cloning vector
OCRR479-OCRR480	BVH-3M	BVH-3 w/oss	21-1039	pSL301
OCRR479-OCRR497	BVH-3AD	BVH-3N ^{end} w/oss	21-509	pSL301
HAMJ248-HAMJ249	L-BVH-3AD	BVH-3N ^{end}	1-509	pET-21(+)
OCRR498-OCRR499	BVH-3B	BVH-3C ^{end}	512-1039	pSL301
OCRR479-HAMJ172	BVH-3C	BVH-3N ^{end} w/oss	21-225	pET-32 α (+)
OCRR487-OCRR488	BVH-11M	BVH-11 w/oss	20-840	pCMV-GH
HAMJ251-OCRR487	BVH-11A	BVH-11N ^{end} w/oss	20-353	pET-32 α (+)

HAMJ171-OCRR488	BVH-	BVH-11 C'end	354-840	pET-32 a(+)
HAMJ264-OCRR488	BVH-	BVH-11 C'end	228-840	pET-32 a(+)
HAMJ278-HAMJ279	NEW1	BVH-3 C'end	472-1039	pET-21b(+)
HAMJ278-HAMJ280	NEW2	BVH-3 C'end	472-800	pET-21b(+)
HAMJ281-HAMJ279	NEW3	BVH-3 C'end	800-1039	pET-21b(+)
HAMJ284-HAMJ285	NEW4	BVH-11 C'end	286-840	pET-21d(+)
HAMJ284-HAMJ286	NEW5	BVH-11	286-713	pET-21d(+)
HAMJ287-HAMJ288	NEW6	BVH-11	672-792	pET-21d(+)
HAMJ285-HAMJ289	NEW7	BVH-11 C'end	709-840	pET-21d(+)
HAMJ284-HAMJ290	NEW8	BVH-11	286-511	pET-21d(+)
HAMJ286-HAMJ291	NEW9	BVH-11	511-713	pET-21d(+)
HAMJ160-HAMJ186	BVH-	BVH-11-2 w/o	20-838	pSL301
HAMJ292-HAMJ293	NEW10	BVH-11-2	271-838	pET-21d(+)
HAMJ293-HAMJ294	NEW11	BVH-11-2	699-838	pET-21d(+)
HAMJ282-HAMJ283	NEW13	BVH-11 C'end	354-840	pET-21b(+)
HAMJ286-HAMJ297	NEW14	BVH-11-2	227-699	pET-21d(+)
HAMJ300-HAMJ313	NEW15	BVH-3 N'end	21-800	pET-21b(+)
HAMJ301-HAMJ302	NEW16	BVH-11 N'end w/o ss	20-709	pET-21d(+)
HAMJ352-HAMJ353	NEW18	BVH-11-2 internal	227-520	pET21d(+)
HAMJ354-HAMJ355	NEW19	BVH-11-2 C'end	497-838	pET21d(+)
HAMJ404-HAMJ279	NEW21	BVH-3 C'end	396-1039	pET21b(+)
HAMJ464-HAMJ465	NEW22	BVH-3 internal	233-446	pET-21a(+)
HAMJ466-HAMJ467	NEW23	BVH-3 internal	398-509	pET-21b(+)
HAMJ352-HAMJ293	NEW24	BVH-11-2 C'end	227-838	pET-21d(+)
HAMJ464-HAMJ470	NEW25	BVH-3 C'end	233-1039	pET-21b(+)
HAMJ278-HAMJ279 (NEW 1) HAMJ282- HAMJ283 (NEW 13)	NEW1 2	Chimera*	M-NEW 1 -KL - NEW 13	pET 21 b (+)
HAMJ284-HAMJ350 (NEW 5) HAMJ351- HAMJ279 (NEW 1)	NEW1 7	Chimera*	M- NEW 5 -GP - NEW 1	pET 21 d (+)
HAMJ358-HAMJ359 (NEW 1) HAMJ403-	NEW2 0	Chimera*	M- NEW 1 -GP - NEW 5	pET 21 d (+)

HAMJ361 (NEW5)				
HAMJ292-HAMJ471 (NEW 10) HAMJ472- HAMJ470(NEW25)	NEW26	Chimera*	M- NEW 10 -GP - NEW25	pET21 d(+)
HAMJ355-HAMJ471 (NEW 19) HAMJ472- HAMJ470(NEW25)	NEW27	Chimera*	M- NEW 19 -GP - NEW25	pET21 d(+)
HAMJ292-HAMJ471 (NEW 10) HAMJ351 - HAMJ279(NEW1)	NEW28	Chimera*	M- NEW 10 -GP - NEW1	pET21 d(+)
HAMJ284-HAMJ350 (NEW 5) HAMJ472- HAMJ470(NEW25)	NEW29	Chimera*	M- NEW 5 -GP - NEW25	pET21 d(+)
HAMJ284-HAMJ483 (NEW 4) HAMJ472- HAMJ470(NEW25)	NEW30	Chimera*	M- NEW 4 -GP - NEW25	pET21 d(+)
HAMJ284-HAMJ483 (NEW 4) HAMJ351- HAMJ279(NEW1)	NEW31	Chimera*	M- NEW 4 -GP - NEW1	pET21 d(+)
HAMJ355-HAMJ471 (NEW 19) HAMJ351- HAMJ279(NEW1)	NEW32	Chimera*	M- NEW 19 -GP - NEW1	pET21 d(+)

w/o ss : without signal sequence. Analysis of the
BVH-3, BVH-11 and BVH-11-2 protein sequences
suggested the presence of putative hydrophobic
5 leader sequences.

* encoded amino acids for the chimeras are expressed
as the gene product, additional non essential amino
acids residue were added M is methionine, K is
lysine, L is leucine, G is glycine and P is proline.

10

Monoclonal antibody (Mab)-secreting hybridomas were obtained by
fusions of spleen cells from immunized mice and non-secreting,
HGPRT-deficient mouse myeloma SP2/0 cells by the methods of
Fazekas De St-Groth and Scheidegger (J Immunol Methods 35 : 1-21,
15 1980) with modifications (J. Hamel et al. J Med Microbiol 23 :
163-170, 1987). Female BALB/c mice (Charles River, St-Constant,
Quebec, Canada) were immunized with either BVH-3M (thioredoxin-
His•Tag-BVH-3M fusion protein/ pET32

system), BVH-11M (thioredoxin-His•Tag-BVH-11M fusion protein/
pET32 system), BVH-11-2M (thioredoxin-His•Tag-BVH-11-2M fusion
protein/ pET32 system), BVH-11B (thioredoxin-His•Tag-BVH-11B
fusion protein/ pET32 system), BVH-3M (His•Tag-BVH-3 fusion
5 protein/ pURV22.HIS system) or NEW1 (NEW1-His•Tag fusion
protein/ pET21 system) gene products from S. pneumoniae strain
SP64 to generate the Mab series H3-, H11-, H112-, H11B-, H3V-,
and HN1-, respectively. Culture supernatants of hybridomas
were initially screened by enzyme-linked-immunoassay (ELISA)
10 according to the procedure described by Hamel et al. (Supra)
using plates coated with preparations of purified recombinant
BVH-3, BVH-11 and/or BVH-11-2 proteins or suspensions of heat-
killed S. pneumoniae cells. The Mab-secreting hybridomas
selected for further characterization are listed in Table 3
15 and Table 4 from the following Example 2. The class and
subclass of Mab immunoglobulins were determined by ELISA
using commercially available reagents (Southern Biotechnology
Associates, Birmingham, AL).

20 Furthermore, the cloning and expression of chimeric gene(s)
encoding for chimeric polypeptides and the protection observed
after vaccination with these chimeric polypeptides are
described.

25 BVH-3 and BVH-11 gene fragments corresponding to the 3' end of
the genes were amplified by PCR using pairs of
oligonucleotides engineered to amplify gene fragments to be
included in the chimeric genes. The primers used had a
restriction endonuclease site at the 5' end, thereby allowing
30 directional in-frame cloning of the amplified product into
digested plasmid vectors (Table 1 and Table 2). PCR-amplified
products were digested with restriction endonucleases and
ligated to linearized plasmid pET21 or pSL301 vector. The
resultant plasmid constructs were confirmed by nucleotide
35 sequence analysis. The recombinant pET21 plasmids containing

a PCR product were linearized by digestion with restriction enzymes for the in-frame cloning of a second DNA fragment and the generation of a chimeric gene encoding for a chimeric pneumococcal protein molecule. Recombinant pSL301 plasmids containing a PCR product were digested with restriction enzymes for the obtention of the DNA inserts. The resulting insert DNA fragments were purified and inserts corresponding to a given chimeric gene were ligated into pET21 vector for the generation of a chimeric gene. The recombinant chimeric polypeptides listed in Table 2 were as C-terminal fusion with an His-tag. The expressed recombinant proteins were purified from supernatant fractions obtained from centrifugation of sonicated IPTG-induced *E. coli* cultures using a His-Bind metal chelation resin (QIAGEN, Chatsworth, CA).

15

Groups of 8 female BALB/c mice (Charles River) were immunized subcutaneously two times at three-week intervals with 25 µg of either affinity purified His•Tag-fusion protein identified in presence of 15-20 µg of QuilA adjuvant. Ten to 14 days following the last immunization, the mice were challenged challenged intravenously with 10E5-10E6 CFU of *S. pneumoniae* type 3 strain WU2. The polypeptides and fragments are capable of eliciting a protective immune response.

25

Table 2A

Experiment	Immunogen	Alive : Dead	Days to death post-infection
1	none	0 : 8	1, 1, 1, 1, 1, 1, 1, 1
	NEW 1	2 : 6	1, 2, 2, 2, 2, 2, >14, >14
	NEW 13	1 : 7	1, 1, 3, 3, 4, 5, 5, >14
	NEW 12	6 : 2	3, 11, 6X >14
	BVH-3M	1 : 7	3, 3, 3, 3, 3, 3, 3, >14
2	none	0 : 8	1, 1, 1, 1, 1, 1, 1, 1

			1
	NEW 17	7 : 1	4, 7 X >14
	NEW 12	3 : 5	3, 3, 3, 4, 5, >14, >14, >14
3	none	0 : 8	2, 2, 2, 2, 2, 2, 2, 2
	NEW 18	1 : 7	2, 2, 2, 2, 3, 3, 3, 3
	NEW 19	8 : 0	8 X >14
	NEW 10	8 : 0	8 X >14
	BVH-11-2	8 : 0	8 X >14

EXAMPLE 2

- 5 This example describes the identification of peptide domains carrying target epitopes using Mabs and recombinant truncated proteins described in example 1.

Hybridomas were tested by ELISA against truncated BVH-3, BVH-11 or BVH-11-2 gene products in order to characterize the epitopes recognized by the Mabs. The truncated gene products were generated from S. pneumoniae SP64 strain except for BVH-3-Sp63 which was generated from S. pneumoniae SP63 strain. As a positive control, the reactivity of each antibody was examined with full-length BVH-3, BVH-11 or BVH-11-2 recombinant proteins. In some cases, the Mab reactivity was evaluated by Western immunoblotting after separation of the gene product by SDS-PAGE and transfer on nitrocellulose paper. The reactivities observed is set forth in the following Table 3 and Table 4.

Table 3. ELISA reactivity of BVH-3-reactive Mabs with a panel of eleven BVH-3 gene products and the BVH-11M molecule

Gene products tested												
Mabs (IgG isotype)	BVH- 3M	BVH- 3AD	BVH- 3B	BVH- 3C	NEW 1	NEW 2	NEW 3	NEW 21	NEW 22	NEW 23	BVH- 3 Sp63	BVH- 11M
H3-4F9 (1)	+	+	-	+	-	-	-	-	-	-	+	+
H3-4D4 (1)	+	+	-	+	-	-	-	-	-	-	+	+
H3-9H12 (1)	+	+	-	+	-	-	-	-	-	-	+	+
H3-7G2 (1)	+	+	-	-	-	-	-	-	+	-	-	-
H3-10A1 (1)	+	+	-	-	-	-	-	+	-	+	+	-
H3-4D3 (1)	+	-	+	-	+	-	+	+	-	-	+	-
H11-6E7 (1)	+	+	-	+	-	-	-	NT	NT	NT	+	+
H11-10H10 (2a)	+	+	-	+	-	-	-	NT	NT	NT	+	+
H11-7G11 (2b)	+	+	+	+	+	+	-	NT	NT	NT	+	+
H3V-4F3 (1)	+	-	+	-	+	-	-	+	-	-	+	-
H3V-2F2 (1)	+	-	+	-	+	+	-	+	-	-	+	-
H3V-7F4 (1)	+	-	+	-	+	+	-	+	-	-	+	-
H3V-7H3 (1)	+	-	+	-	+	-	+	+	-	-	+	-

Gene products tested													
Mabs (IgG isotype)	BVH- 3M	BVH- 3AD	BVH- 3B	BVH- 3C	NEW 1	NEW 2	NEW 3	NEW 21	NEW 22	NEW 23	BVH- 3 Sp63	BVH- 11M	
H3V-13B8 (1)	+	-	+	-	+	-	+	+	-	-	+	-	
H3V-9C2 (1)	+	+	-	+/ -	-	-	-	-	+	-	+/ -	+/ -	
H3V-9C6 (1)	+	+	-	-	-	-	-	-	+	-	-	-	
H3V-16A7 (1)	+	+	-	-	-	-	-	+	-	+	-	-	
H3V-15A10 (1)	+	+	+	+/ -	+	+	-	+	+	+	+	+/ -	
H3V-6B3 (1/2)	+	+	NT	NT	+	+	-	+	+	-	NT	-	
HN1-5H3 (2b)	+	-	+	NT	+	-	-	+	-	-	+	-	
HN1-8E3 (2a)	+	-	+	NT	+	-	-	+	-	-	+	-	
HN1-14F6 (2a)	+	-	+	NT	+	-	-	+	-	-	+	-	
HN1-2G2 (1)	+	-	+	NT	+	+	-	+	-	-	+	-	

Mabs (IgG isotype)	Gene products tested											
	BVH- 3M	BVH- 3AD	BVH- 3B	BVH- 3C	NEW 1	NEW 2	NEW 3	NEW 21	NEW 22	NEW 23	BVH- 3 Sp63	BVH- 11M
HN1-12D8 (2a)	+	-	+	NT	+	+	-	+	-	-	+	-
HN1-14B2 (2a)	+	-	+	NT	+	+	-	+	-	-	+	-
HN1-1G2 (2a)	+	-	+	NT	+	-	+	+	-	-	+	-
HN1-10C12 (1)	+	-	+	NT	+	-	+	+	-	-	+	-
HN1-3E5 (1)	+	+	-	-	+	+	+	+	-	+	+	-

NT : not tested

+/- : very low reactivity but higher than background, possible non-specific Mab binding

Table 4. ELISA reactivity of BVH-11 and/or BVH-11-2-reactive Mabs with a panel of fourteen BVH-11 and BVH-11-2 gene products and the BVH-3M molecule

Gene products tested																
Mabs (IgG isotype)	BVH- 11M	BVH- 11A	BVH- 11B	BVH- 11C	NEW 5	NEW 6	NEW 7	NEW 8	NEW 9	NEW 10	NEW 11	NEW 14	NEW 18	NEW 19	BVH- 11- 2-M	BVH- 3M
H3-4F9 (1)	+	+	-	-	-	-	-	-	-	-	-	-	-	-	+	+
H3-4D4 (1)	+	+	-	-	-	-	-	-	-	-	-	-	-	-	+	+
H3-9H12 (1)	+	+	-	-	-	-	-	-	-	-	-	-	-	-	+	+
H11-6E7 (1)	+	+	-	-	-	-	-	-	-	-	-	-	-	-	+	+
H11- 10H10 (2a)	+	+	-	-	-	-	-	-	-	-	-	-	-	-	+	+
H11-7G11 (2b)	+	+	-	-	-	-	-	-	-	-	-	-	-	-	+	+
H11-1B12 (1)	+	+	-	-	-	-	-	-	-	-	-	-	-	-	+	-
H11-7B9	+	+	-	-	-	-	-	-	-	-	-	-	-	-	+	-

Gene products tested																
Mabs (IgG isotype)	BVH- 11M	BVH- 11A	BVH- 11B	BVH- 11C	NEW 5	NEW 6	NEW 7	NEW 8	NEW 9	NEW 10	NEW 11	NEW 14	NEW 18	NEW 19	BVH- 11- 2-M	BVH- 3M
(2a)																
H11-3H5 (1)	+	-	+	+	+	-	-	-*	-	+	-	+	+	-	+	-
H11-10B8 (1)	+	-	+	+	+	-	-	-*	-	+	-	+	+	-	+	-
H11-1A2 (1)	+	-	+	+	+	-	-	-*	-	+	-	+	+	-	+	-
H112-3A1 (1)	+	-	+	NT	+	-	-	+	-	+	-	+	+	-	+	-
H112- 13C11 (1)	+	+/-	+	NT	+	-	-	+	-	+	-	+	+	-	+	-
H112- 10H10 (1)	+	+	-	NT	+	-	-	+	-	+	-	+	+	-	+	-
H112-1D8 (2a)	+	+	-	NT	+	-	-	+	-	+	-	+	+	-	+	-

45

Gene products tested																
Mabs (IgG isotype)	BVH- 11M	BVH- 11A	BVH- 11B	BVH- 11C	NEW 5	NEW 6	NEW 7	NEW 8	NEW 9	NEW 10	NEW 11	NEW 14	NEW 18	NEW 19	BVH- 11- 2-M	BVH- 3M
10C5 (1)																
H112- 14H6 (1)	-	-	-	NT	-	-	-	-	-	+	+	-	-	+	+	-
H112-7G2 (1)	-	-	-	NT	-	-	-	-	-	+	-	+	+	-	+	-
H112- 13H10 (2a)	-	-	-	NT	-	-	-	-	-	-	-	+	+	-	+	-
H112-7E8 (2b)	+/-	-	-	NT	-	-	-	-	-	-	-	-	+/-	-	+	-
H112-7H6 (1)	+/-	-	-	NT	-	-	-	-	-	+/-	-	-	-	-	+	-
H11B- 5F10 (1)	+	-	+	+	+	-	-	+	-	+	-	+	+	-	+	-
H11B- 15G2 (1)	+	-	+	+	+	-	-	+	-	+	-	+	+	-	+	-
H11B-	+	-	+	+	+	-	-	-	+	+	-	+	-	+	+	-

	Gene products tested															BVH- 11M	BVH- 11A	BVH- 11B	BVH- 11C	NEW 5	NEW 6	NEW 7	NEW 8	NEW 9	NEW 10	NEW 11	NEW 14	NEW 18	NEW 19	BVH- 11- 2-M	BVH- 3M
Mabs (IgG isotype)																															
13D5 (2)																															
H11B- 11B8 (1)	+	-	+	+	+	-	-	-	-	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	-			
H11B- 7E11 (1)	+	-	+	+	+	-	-	-	-	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	-			
H11B-1C9 (1)	+	-	+	+	+	-	-	-	-	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	-			
H11B-5E3 (2)	+	-	+	+	+	-	-	-	-	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	-			
H11B-6E8 (1)	+	-	+	+	+	-	-	-	-	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	-			

NT : not tested

+/- : very low reactivity but higher than background, possible non-specific Mab binding

* : a strong signal was detected when tested by Western immunoblotting

The deduced locations of the epitopes are summarized in Figure 28 and Figure 29. As can be seen from the data in Table 3, BVH-3-reactive Mabs can be divided into two groups : BVH-3A- and BVH-3B-reactive Mabs with the exception of Mabs H11-7G11 and H3V-15A10 which reacted with both, BVH-3A and BVH-3B molecules. The BVH-3A-reactive Mabs can be subdivided in two subgroups of antibodies depending of their reactivity or lack of reactivity with BVH-3C recombinant protein. Mab reactive with BVH-3C protein recognized epitopes shared by both, BVH-3 and BVH-11 proteins. As can be seen in Table 4, these BVH-3- and BVH-11-cross-reactive Mabs were also reactive with BVH-11A and BVH-11-2M recombinant proteins. BVH-3B-reactive Mabs can be subdivided into three subgroups according to their reactivity with NEW1, NEW2 and NEW3 recombinant proteins. Some Mabs were only reactive with the NEW1 protein while other Mabs were reactive with either, NEW1 and NEW2 or NEW1 and NEW3 recombinant proteins.

Mabs H11-7G11 and H3V-15A10 react with epitopes in more than one position on BVH-3. The reactivity of H11-7G11 with BVH-3AD, BVH-3B, BVH-3C, BVH-11A and BVH-11-2M molecules suggests that H11-7G11 epitope might comprised HXXHXXH sequence. This sequence is repeated, respectively, 6 and 5 times in BVH-3 and BVH-11/BVH-11-2 protein sequences. The lack of reactivity of Mab H11-7G11 with NEW 10 molecule suggests that the epitope includes the HGDHXXH sequence. Multiple-position mapping of H3V-15A10 epitope on BVH-3 is suggested by the reactivity of the Mab with two BVH-3 fragments that do not overlap.

Interestingly, Mabs H3-7G2, H3V-9C6 and H3V-16A7 were not reactive with BVH-3 Sp63 thus allowing the location of their corresponding epitopes on a 177-amino acid fragment comprised between amino acids 244 and 420 on BVH-3 molecule of S. pneumoniae SP64 (Figure 31).

As can be seen from the data in Table 4, the Mabs that are reactive with BVH-11- and/or BVH-11-2 and that do not recognize BVH-3 molecules can be divided into three groups according to their reactivities with BVH-11A and NEW10 recombinant proteins. Some Mabs reacted exclusively with either BVH-11A or NEW10 protein while other Mabs were reactive with both, BVH-11A and NEW10 recombinant proteins.

10 EXAMPLE 3

This example describes the construction of BVH-3 and BVH-11-2 gene libraries for the mapping of epitopes.

15 BVH-3 and BVH-11-2 gene libraries were constructed using recombinant pCMV-GH and PSL301 plasmid DNA containing respectively, BVH-3 gene sequence spanning nucleotides 1837 to 4909 (SEQ ID NO: 2) or BVH-11-2 gene sequence spanning nucleotides 172 to 2630 (SEQ ID NO: 5) and the Novatope® library construction and screening system (Novagen). The recombinant plasmids containing BVH-3 or BVH-11-2 gene fragment were purified using QIAGEN kit (Chatsworth, CA) and digested with the restriction enzymes BglII and XbaI respectively. The resulting BglII-XbaI DNA fragments were purified using the QIAquick gel extraction kit from QIAGEN and digested with Dnase I for the generation of randomly cleaved DNA. DNA fragments of 50 to 200 bp were purified, treated with T4 DNA polymerase to blunt the target DNA ends and add a single 3'dA residue, and ligated into pSCREEN-T-Vector (Novagen) following the procedures suggested by the manufacturer (Novatope® System, Novagen). The gene libraries of E. coli clones, each of which expressing a small peptide derived from BVH-3 or BVH-11-2 genes were screened by standard colony lift methods using Mabs as immunoprobosc. The colony screening was not successful with Mabs producing very high backgrounds on colony lifts. Moreover, in some cases, Mabs

failed to detect epitope-expressing-colonies. The lack of reactivity can possibly be explained by the small amount of recombinant proteins produced or the recognition of conformation-dependent epitopes consisting of different protein domains. Sequencing of DNA inserts from positive clones determined the location of the segment that encodes the target epitope. The data are presented in Table 5. The peptides encoded by DNA inserts into the recombinant pSCREEN-T vector can be purified and used as immunogens as described below in Example 6.

The peptide sequences obtained from the screening of BVH-3 and BVH-11-2 gene libraries with the Mabs are in agreement with the Mab ELISA reactivities against the truncated gene products. As expected, the amino acid sequences obtained from H11-7G11 contained the sequence HGDHXXH. These findings provide additional evidence for the location of epitopes recognized with the Mabs. Interestingly, although the Mabs H112-10G9, H112-10A2 and H11B-11B8 were reactive against the same peptide sequence (amino acid residues 594 to 679 on BVH-11-2 protein sequence), clones corresponding to the sequence spanning from amino acid residues 658 to 698 were only picked up by Mab H11B-11B8 thus revealing the location of H11B-11B8 epitope between amino acid residues 658 to 679 (SEQ ID NO: 163). Mabs H112-10G9, H112-10A2, and H11B-11B8 are directed against 3 distinct non overlapping epitopes located closely on the peptide sequence corresponding to amino acid residues 594 to 679 (SEQ ID NO: 22).

30

Table 5. Peptide sequences obtained from the screening of BVH-3 and BVH-11-2 gene libraries with
Mabs

Mab	Clone/ Protein designat ion	Nucleotide position	Amino acid position	Amino acid sequence	SEQ ID NO
H3-4D4	4D4.9	SEQ ID 1: 226-509	SEQ ID 6: 76-169	DQGYVTSHGHDHYHYNGKVPYDALFSEELMKDPNVQLKDA DIVNEVKGGYIIKVDGKYVYVLKDAAHADNVRTKDEINRQK QEHVKDNEKVN	11
H11- 7G11	7G11.7	SEQ ID 1: 193-316	SEQ ID 6: 64-105	GIQAEQIVIKITDQGYVTSHGHDHYHYNGKVPYDALFSEEL L	12
H11- 7G11	7G11.9	SEQ ID 1: 1171-1284	SEQ ID 6: 390-428	TAYIVRHGDHFIYIPKSNQIQOPTLPNNSLATPSPSLPI	13
H3-4D3	4D3.4	SEQ ID 1: 2565-2670	SEQ ID 6: 855-890	TSNSTLEEVPVTPVQEKVAKFAESYGMKLENVLFN	14
HN1- 8E3	8E3.1	SEQ ID 1: 3004-3120	SEQ ID 6: 1016-1039	MDGTIELRLPSGEVIKKNLSDFIA	15
HN1- 1G2	1G2.2	SEQ ID 1: 3017-3120	SEQ ID 6: 1005-1039	YGLGLDSVIFNMDGTIELRLPSGEVIKKNLSDFIA	16
HN1- 10C12	10C12.7	SEQ ID 1: 2936-3120	SEQ ID 6: 983-1039	PALEEAPAVDPVQEKLEKFTASYGLGLDSVIFNMDGTIELR LPSGEVIKKNLSDFIA	17
HN1- 14F6	14F6.3	SEQ ID 1: 2501-2618	SEQ ID 6: 833-872	KVEEPTSEKVEKEKLSETGNSTNSTLEEVPVTPVQEK	18

Mab	Clone/ Protein designat ion	Nucleotide position	Amino acid position	Amino acid sequence	SEQ ID NO
HN1- 12D8	B12D8.2	SEQ ID 1:1433- 1767	SEQ ID 6: 512-589	MKDLKKIEKIAIMQYGVKRESIVVNKEKNALIIYPHGD HHHADPIDEHKPVGIGHSHSNYELFKPEEGVAKKEGN	19
H3V- 7F4	7F4.1	SEQ ID 1: 1633-1785	SEQ ID 6: 545-595	AIYPHGDHHHADPIDEHKPVGIGHSHSNYELFKPEEGVAK KEGNKVYTGE	20
H112- 10D7	10D7.5	SEQ ID 5: 1685-1765	SEQ ID 8: 525-553	IQVAKLAGKYTTEDGYIFDPRDITSDEGD	21
H112- 10G9	10G9.3	SEQ ID 5: 1893-2150	SEQ ID 8: 594-679	DHQDSGNTAEAKGAEAIYNRVKAACKVPLDRMPYNLQYTVEV KNGSLIIPHYDHYHNIKFEWFDEGLYEAPKGYSLEDLLATV KYYV	22
H112- 10A2	10A2.2	SEQ ID 5: 1893-2150	SEQ ID 8: 594-679	DHQDSGNTAEAKGAEAIYNRVKAACKVPLDRMPYNLQYTVEV KNGSLIIPHYDHYHNIKFEWFDEGLYEAPKGYSLEDLLATV KYYV	22
H11B- 11B8	B11B8.1	SEQ ID 5: 1893-2150	SEQ ID 8: 594-679	DHQDSGNTAEAKGAEAIYNRVKAACKVPLDRMPYNLQYTVEV KNGSLIIPHYDHYHNIKFEWFDEGLYEAPKGYSLEDLLATV KYYV	22
H11B- 11B8	11B8.4	SEQ ID 5: 2085-2217	SEQ ID 8: 658-698	GLYEAPKGYSLEDLLATVKYYVVEHPNERPHSDNFGFNASDH	23

Mab	Clone/ Protein designat ion	Nucleotide position	Amino acid position	Amino acid sequence	SEQ ID NO
H112- 3A4	3A4.1	SEQ ID 5: 2421-2626	SEQ ID 8: 769-837	VENSVINAKIADAEALLEKVTDPsirQNAMETLTGLKSSLL LGTKDNNNTISAEVDSLLALLKESQPAPI	24

EXAMPLE 4

This example describes the immunization of animals with recombinant proteins for the generation of antibody reactive
5 with BVH-3, BVH-11 and/or BVH-11-2.

NZW rabbits (Charles River Laboratories, St-Constant, Québec, Canada) were immunized subcutaneously at multiple sites with 50 µg or 100 µg of the purified BVH-3M, L-BVH-3AD, NEW1,
10 NEW13, or L-BVH-11 recombinant protein in presence of 80 µg of QuilA adjuvant (Cedarlane Laboratories Ltd, Hornby, Canada). The rabbits were boosted two times at three-week intervals with the same antigen and blood samples were collected before each immunization and 6 to 28 days following
15 the last immunization. The sera samples were designated preimmune, post 1st, post 2nd or post 3rd injection. The rabbit immune response to immunization was evaluated by ELISA using recombinant BVH-3M (BVH-3M-His•Tag fusion protein/ pET21 system) or BVH-11M (BVH-11M-His•Tag fusion protein/ pET21
20 system) proteins or suspensions of heat-killed S. pneumoniae Rx-1 cells as coating antigens. ELISA titer was defined as the reciprocal of the highest sera dilution at which absorbance A₄₁₀ value was 0.1 above the background value. Antibodies reactive with BVH-3 and/or BVH-11 epitopes were
25 elicited following immunization in all animals as shown in the following Table 6. Antibody reactive with recombinant or pneumococcal antigens was not present in the preimmune sera. The immune response to immunization was detectable in the sera of each rabbit after a single injection of recombinant
30 antigen. The antibody response following the second injection with either antigen tested was characterized by a strong increase in antibody titer. Interestingly, good titers of antibody reactive with S. pneumoniae cells, with an average titer of 52,000 after the third immunization, were obtained,
35 thus establishing that native pneumococcal epitopes are expressed on the recombinant E. coli gene products. These

data support the potential use of BVH-3, BVH-11 and/or BVH-11-2 gene products and the antibody raised to BVH-3, BVH-11 and/or BVH-11-2 gene products as vaccines for the prevention and the treatment of pneumococcal disease, respectively.

- 5 Table 6. Rabbit Antibody response to immunization with BVH-3 and BVH-11 gene products

Rabbit	Immunogen	Sera sample	ELISA Titer with coating antigen		
			BVH-3M	BVH-11M	<u>S. pneumoniae</u>
#15	BVH-3M (50µg)	Preimmune	NT	NT	200
		Post-1 st	NT	NT	1,600
		Post-2 nd	NT	NT	20,000
		Post-3 rd	512,000	NT	40,000
#16	BVH-3M (100µg)	Preimmune	NT	NT	200
		post 1 st	NT	NT	1,600
		post 2 nd	NT	NT	40,000
		post 3 rd	10 ⁶	NT	80,000
#112	L-BVH-3AD (50 µg)	Preimmune	<100	NT	NT
		post 1 st	16,000	NT	NT
		post 2 nd	512,000	NT	NT
		post 3 rd	2x10 ⁶	NT	32,000
#113	New 1 (50 µg)	Preimmune	<100	NT	NT
		post 1 st	16,000	NT	NT
		post 2 nd	512,000	NT	NT
		post 3 rd	10 ⁶	NT	64,000
#114	New 13 (50 µg)	Preimmune	NT	<100	NT
		post 1 st	NT	16,000	NT
		post 2 nd	NT	64,000	NT
		post 3 rd	NT	256,000	32,000
		Preimmune	NT	<100	NT

#116	L-BVH-11 (50 µg)	post 1 st	NT	64,000	NT
		post 2 nd	NT	10 ⁶	NT
		post 3 rd	NT	2x10 ⁶	64,000

NT : not tested

EXAMPLE 5

- 5 This example describes the protection of animals against fatal experimental pneumococcal infection by administration of antibody raised to BVH-3, BVH-11 or BVH-11-2 gene products.
- 10 High-titer Mab preparations were obtained from ascites fluid of mice inoculated intraperitoneally with Mab-secreting hybridoma cells according to the method described by Brodeur et al (J Immunol Methods 71 :265-272, 1984). Sera samples were collected from rabbits immunized with BVH-3M as described
- 15 in Example 4. The rabbit sera collected after the third immunization and ascites fluid were used for the purification of antibodies by precipitation using 45 to 50% saturated ammonium sulfate. The antibody preparations were dissolved and dialyzed against phosphate-buffered saline (PBS).
- 20 CBA/N (xid) mice (National Cancer Institute, Frederick, MA) were injected intraperitoneally with either 0.1 ml of purified rabbit antibodies or 0.2 ml of ascites fluid before intravenous challenge with approximately 200 CFU of the type 3
- 25 S. pneumoniae strain WU2. Control mice received sterile PBS or antibodies purified from preimmune rabbit sera or sera from rabbits immunized with an unrelated N. meningitidis recombinant protein antigen. One group of mice was challenged with S. pneumoniae before the administration of anti-BVH-3
- 30 antibody. Samples of the S. pneumoniae challenge inoculum were plated on chocolate agar plates to determine the number of CFU and verify the challenge dose. The CBA/N mice were chosen because of their high susceptibility to S. pneumoniae

infection. The LD₅₀ of WU2 injected intravenously to CBA/N mice is estimated to be ≤10 CFU. Deaths were recorded at 24-h intervals for a period of at least 7 days.

- 5 The protection data obtained from mice injected with rabbit anti-BVH-3 antibody are set forth in the following Table 7. Nine out of 10 mice receiving the anti-BVH-3 antibody survived the challenge in contrast to none of 10 mice injected with control antibody or PBS buffer. The observation that antibody
- 10 raised to the BVH-3-M molecule passively protected even when administered after the challenge demonstrated the ability of anti-BVH-3 antibody to prevent death even from an already established infection.
- 15 Table 7. Protective effects of rabbit antibody to BVH-3-M gene in CBA/N mice challenged i.v. with WU2 pneumococci

Antibody preparation	Time of antibody administration	Alive : Dead	Days to death post-infection
Anti-BVH3M	1 h before infection	5 : 0	>14, >14, >14, >14, >14
Anti-N. meningitidis	1 h before infection	0 : 5	2, 2, 2, 2, 2
Anti-BVH-3M	0.5 h post-infection	4 : 1	2, >14, >14, >14, >14
None (PBS)	1 h before infection	0 : 5	1, 2, 2, 2, 2

CBA/N mice were infected with 1000 CFU of WU2 S. pneumoniae before or after intraperitoneal administration of 0.1 ml of rabbit antibody.

20

In an other experiment, 0.1 ml of rabbit antibody prepared from preimmune and immune sera were administered intraperitoneally to CBA/N mice four hours before intranasal challenge with 280 CFU of S. pneumoniae P4241 type 3 strain.

- 25 As seen in the following Table 8, all immunized mice survived

the challenge while none of 9 mice receiving preimmune sera antibody or buffer alone were alive on day 6 post-infection. S. pneumoniae hemocultures on day 11 post-challenge were negative for all surviving mice. Furthermore, 100% protection was observed in mice receiving monoclonal antibodies H112-10G9 or a mixture of H112-10G9 and H11B-7E11 which are directed against BVH-11/BVH-11-2.

- 10 Table 8. Protective effects of passive transfer of rabbit antibody to BVH-3-M gene product or anti-BVH-11/BVH-11-2 specific Mabs in CBA/N mice challenged i.n. with P4241 pneumococci

Antibody preparation	Alive : Dead	Days to death post-infection
Anti-BVH-3M	5 : 0	>11, >11, >11, >11, >11
Antibody from preimmune sera	0 : 5	3, 3, 3, 6, 6
H112-10G9	4 : 0	>11, >11, >11, >11
H112-10G9+H11B- 7E11	5 : 0	>11, >11, >11, >11, >11
None (PBS)	0 : 4	3, 3, 3, 3

15

Altogether, the results from Table 7 and Table 8 clearly establish that immunization of animals with a BVH-3 gene product such as BVH-3M elicited protective antibodies capable of preventing experimental bacteremia and pneumonia infections.

20

The protection data obtained for mice injected with ascites fluid are set forth in the following Table 9. Administration of a volume of 0.2 ml of ascites fluid of 0.2 ml of some sets of ascites fluid prevented death from experimental infection. For example, H112-3A4 + H112-10G9 and H112-10G2 + H112-10D7

25

sets of 2 Mabs conferred complete protection against experimental infection. These data indicated that antibody targetting BVH-11 and/or BVH-11-2 epitopes gave efficient protection. The Mabs H112-3A4, H112-10G9, H112-10D7, H112-10A2, H112-3E8, H112-10C5, H11B-11B8, H11B-15G2, H11B-1C9, H11B-7E11, H11B-13D5 and H11-10B8 were present in at least one protective pair of Mabs and were said to be protective and reactive against protective epitopes. The locations of protection-conferring epitopes on BVH-11-2 molecules are summarized in Table 10 and Figure 29 . Protective Mabs H112-3A4, H112-10G9, H112-10D7, H112-10A2, H112-3E8, H112-10C5, H11B-11B8, H11B-15G2, H11B-1C9, H11B-7E11, H11B-13D5 and H11-10B8 were all reactive with New 10 protein corresponding to amino acid residues 271 to 838 on the BVH-11-2 molecule. Six out of these 12 Mabs were directed against epitopes present in the NEW 19 protein and 3 protective Mabs recognized NEW 14. Interestingly, Mab H112-3A4 and H112-10C5 reacted with distinct epitopes exclusive to BVH-11-2 located at the carboxyl end comprised between amino acid residues 769 and 837. Also, Mabs H11-7G11, H11-6E7 and H3-4F9 reactive with epitopes shared by pneumococcal BVH-3, BVH-11 and BVH-11-2 molecules did not succeed to protect even if given in combination with protective H112-10G9 or H112-11B8 Mab. These Mabs recognized epitopes located at the amino end of the BVH-3, BVH-11 and BVH-11-2 molecules comprising, respectively, the first 225, 228 and 226 amino acid residues. The comparison of the BVH-3, BVH-11 and BVH-11-2 protein sequences revealed that a large number of amino acids were conserved in the amino end portion comprising these 225-228 residues with a global 72.8 % identity (Figure 32).

Altogether the data set forth in Table 9 and Table 10 suggest that the protection eliciting BVH-11- and BVH-11-2-epitopes is comprised in the carboxy terminal product containing amino acids 229 to 840 and 227 to 838, on BVH-11 and BVH-11-2 proteins, respectively.

Table 9. Passive immunization with BVH-11- and/or BVH-11-2-specific Mabs can protect mice from lethal experimental pneumococcal infection.

Experiment	Mab	Alive : Dead	Days to death post-infection
1	H112 3A4 + H112-10G9	6 : 0	6 X >10
	H112-3A4 + H112-10D7	5 : 1	4, 5X >10
	None	0 : 6	2, 2, 2, 2, 2, 6
2	H112-10 A2 + H112-10D7	5 : 1	3, 5X >10
	H112-3E8 + H112-10G9	6 : 0	6 X >10
	None	0 : 6	2, 2, 2, 2, 2, 2
3	H112-10D7 + H11B-11B8	6 : 0	6 X >10
	H112-10G9 + H11B-15G2	3 : 3	2, 6, 6, 3 X >10
	None	0 : 6	2, 2, 2, 2, 2, 2
4	H112-10G9 + H112-10D7	5 : 0	5 X >11
	None	0 : 5	2, 2, 2, 2, 2
5	H112-10G9 + H11-10B8	4 : 1	8, 4 X >14
	H112-10G9 + H11B-7E11	5 : 0	5 X >14
	None	0 : 3	1, 2, 2
6	H112-10G9 + H11B-1C9	4 : 1	4, 4 X >14
	None	0 : 3	2, 2, 2
7	H112-10C5 + H11B-13D5	5 : 0	5 X >14
	None	3 : 3	2, 2, 2

- 5 CBA/N mice were injected intraperitoneally with a total of 0.2 ml of ascites fluid 4 hours before intravenous challenge with S. pneumoniae WU2.

Table 10. Deduced locations of protection-conferring epitopes on BVH-11-2 molecules.

Mabs	Protection	Gene products carrying Mab-epitope
H112-3A4	+	NEW 19 and NEW 11
H112-10G9	+	NEW 19
H112-10D7	+	NEW 14 and NEW 10
H112-10A2	+	NEW 19
H112-3E8	+	NEW 19
H11B-11B8	+	NEW 19
H11B-15G2	+	NEW 18
H11B-7E11	+	NEW 14 and NEW 10
H11-10B8	+	NEW 18
H11B-1C9	+	NEW 14 and NEW 10
H112-3A1	-	NEW 18 and NEW 8
H112-10H10	-	NEW 18 and NEW 8
H112-2H7	-	BVH-11-2M
H112-6H7	-	BVH-11-2M
H11-7G11	-	BVH-11A and BVH-3C
H11-6E7	-	BVH-11A and BVH-3C
H112-10C5	+	NEW 19, NEW11 and 3A4.1
H11B-13D5	+	NEW 19
H112-7G2	-	NEW 18
H112-7E8	-	BVH-11-2M
H3-4F9	-	BVH-11A and BVH-3C

- 5 Altogether the data presented in this example substantiate the potential use of antibodies raised to BVH-3, BVH-11 or BVH-11-2 molecules as therapeutic means to prevent, diagnose or treat S. pneumoniae diseases.

10 EXAMPLE 6

This example describes the localization of surface-exposed peptide domains using Mabs described in Example 1.

S. pneumoniae type 3 strain WU2 was grown in Todd Hewitt (TH) broth (Difco Laboratories, Detroit MI) enriched with 0.5% Yeast extract (Difco Laboratories) at 37°C in a 8% CO₂ atmosphere to give an OD₆₀₀ of 0.260 (~10⁸ CFU/ml). The bacterial suspension was then aliquoted in 1 ml samples and the S. pneumoniae cells were pelleted by centrifugation and resuspended in hybridoma culture supernatants. The bacterial suspensions were then incubated for 2 h at 4°C. Samples were washed twice in blocking buffer [PBS containing 2% bovine serum albumin (BSA)], and then 1 ml of goat fluorescein (FITC)-conjugated anti-mouse IgG + IgM diluted in blocking buffer was added. After an additional incubation of 60 min at room temperature, samples were washed twice in blocking buffer and fixed with 0.25 % formaldehyde in PBS buffer for 18-24 h at 4°C. Cells were washed once in PBS buffer and resuspended in 500 µl of PBS buffer. Cells were kept in the dark at 4°C until analyzed by flow cytometry (Epics® XL; Beckman Coulter, Inc.). Ten thousands (10,000) cells were analyzed per sample and the results were expressed as % Fluorescence and Fluorescence index (FI) values. The % Fluorescence is the number of fluorescein-labelled S. pneumoniae cells divided by 100 and the FI value is the median fluorescence value of pneumococci treated with Mab supernatant divided by the fluorescence value of pneumococci treated with the conjugate alone or with a control unrelated Mab. A FI value of 1 indicated that the Mab has not been detected at the surface of the bacteria whereas a FI value higher than 2 was considered positive when at least 10 % of the pneumococcal cells were labelled and indicated that the Mab was reactive with cell-surface exposed epitopes. The following Table 11 summarized the data obtained with the Mabs tested by flow cytometry.

Flow cytometric analysis revealed that the Mabs reactive with BVH-3C and/or BVH-11A molecules did not bind to the cell surface. In contrast, with the exception of Mabs H3V-9C6 and H3V-16A7, the Mabs reactive with NEW 1, NEW 2, NEW 3, NEW 22 or NEW 23 BVH-3 gene products were detected at the surface of pneumococci. These data indicated that the first 225 amino acid residues located at the amino end of BVH-3 are internal. The lack of binding of Mabs H3V-9C6 and H3V-16A7 suggest some portions of the sequence corresponding to the 177-amino acids absent from the BVH-3 molecule of S. pneumoniae SP63 appears not to be accessible to antibodies.

Results from BVH-11- and/or BVH-11-2-reactive Mabs revealed that there is a good correlation between surface-exposure and protection. All Mabs reactive with internal epitopes as determined by the flow cytometry assay were not protective whereas all the protective Mabs described in Example 5 gave a positive signal in flow cytometry. Although an FI value of 9.0 and a % Fluorescence of 81.2 were obtained with Mab H11-7G11, this Mab was not shown to protect. Additional assays can be used to further evaluate whether this Mab and its corresponding epitope might participate in anti-infectious immunity.

Table 11. Results from the binding of Mabs at the surface of S. pneumoniae by flow cytometry analysis

Mab	% Fluorescence	FI	Binding	Gene products carrying Mab-epitope
H3-4F9	3.4	1.2	-	BVH-3C and BVH-11A
H3-4D4	3.4	1.2	-	BVH-3C and BVH-11A
H3-9H12	2.5	1.1	-	BVH-3C and BVH-11A
H3-7G2	66.2	6.3	+	NEW 22
H3-10A1	58.8	5.6	+	NEW 23

Mab	% Fluorescence	FI	Binding	Gene products carrying Mab-epitope
H3-4D3	33.2	3.5	+	NEW 3
H3V-4F3	24.4	2.9	+	NEW 1
H3V-2F2	15.6	2.4	+	NEW 2
H3V-7F4	58.7	5.6	+	NEW 2
H3V-7H3	68.8	6.9	+	NEW 3
H3V-13B8	75.0	7.7	+	NEW 3
H3V-9C2	66.4	6.2	+	NEW 22
H3V-9C6	2.9	1.0	-	NEW 22
H3V-16A7	6.6	1.7	-	NEW 23
H3V-15A10	58.7	5.7	+	NEW 22 and NEW 23
HN1-5H3	43.4	5.3	+	NEW 1
HN1-8E3	57.4	6.6	+	NEW 1
HN1-14F6	57.8	6.7	+	NEW 1
HN1-2G2	54.8	6.3	+	NEW 2
HN1-12D8	14.3	3.0	+	NEW 2
HN1-14B2	11.5	2.7	+	NEW 2
HN1-1G2	59.9	7.0	+	NEW 3
HN1-10C12	13.6	2.8	+	NEW 3
H11-6E7	4.9	1.2	-	BVH-3C and BVH-11A
H11-10H10	6.5	1.6	-	BVH-3C and BVH-11A
H11-7G11	81.2	9.0	+	BVH-3C and NEW 2
H11-1B12	3.1	1.2	-	BVH-11A
H11-7B9	2.4	1.1	-	BVH-11A
H11-10B8	81.1	9.1	+	NEW 18 and NEW 8
H11-1A2	84.4	10	+	NEW 18 and NEW 8
H11-3H5	84.0	9.8	+	NEW 18 and NEW 8
H112-13C11	49.3	5.9	+	NEW 18 and NEW 8
H112-	0.4	1.0	-	BVH-11A and NEW 18

Mab	% Fluorescence	FI	Binding	Gene products carrying Mab-epitope
10H10				
H112-1D8	0.4	1.0	-	BVH-11A and NEW 18
H112-10G9	78.9	10.4	+	NEW 19
H112-10A2	75.5	9.6	+	NEW 19
H112-3E8	62.5	7.5	+	NEW 19
H112-10D7	64.5	7.7	+	NEW 14
H112-2H7	0.7	1.1	-	BVH-11A
H112-6H7	0.3	1.0	-	BVH-11A
H112-3A4	70.1	8.9	+	NEW 11
H112-10C5	86.3	9.2	+	NEW 11 AND 3A4.1
H112-14H6	89.6	11	+	NEW 11
H112-14H6	0.8	1.4	-	NEW 11
H112-7G2	4.7	2.0	-	NEW 18
H112-13H10	0.5	1.0	-	NEW 18
H112-7E8	0.4	1.0	-	BVH-11-2M
H112-7H6	0.2	1.0	-	BVH-11-2M
H11B-5F10	3.1	1.1	-	NEW 18
H11B-15G2	60.2	5.7	+	NEW 18 and NEW 8
H11B-13D5	75.7	8.3	+	NEW 19
H11B-11B8	78.4	8.3	+	NEW 19
H11B-	32.3	3.5	+	NEW 14

Mab	% Fluorescence	FI	Binding	Gene products carrying Mab-epitope
7E11				
H11B-1C9	57.3	5.5	+	NEW 14
H11B-5E3	1.8	1.0	-	NEW 7
H11B-6E8	2.4	1.0	-	NEW 7

EXAMPLE 7

- 5 This example describes the immunization of animals with peptide epitopes of BVH-3 and BVH-11-2.

The recombinant pSCREEN-T vector (Novagen, Madison, WI) containing DNA fragment (nucleotides 2421 to 2626 on SEQ ID NO : 5), encoding the Mab 3A4-epitope (SEQ ID NO: 24) was transformed by electroporation (Gene Pulser II apparatus, BIO-RAD Labs, Mississauga, Canada) into *E. coli* Tuner (λ DE3) pLysS [BL21 (F' ompT hsdSB (rB⁻mB⁻) gal dcm lacYI pLysS (Cm^r)] (Novagen). In this strain, the expression of the fusion protein is controlled by the T7 promoter which is recognized by the T7 RNA polymerase (present on the λ DE3 prophage, itself under the control of the lac promoter inducible by isopropyl- β -D-thiogalactopyranoside (IPTG). The pLysS plasmid reduces the basal fusion protein expression level by coding for a T7 lysozyme, which is a natural inhibitor of the T7 RNA polymerase.

The transformants were grown at 37°C with 250 RPM agitation in LB broth (peptone 10g/l, yeast extract 5g/l, NaCl 5g/l) supplemented with 50mM glucose, 100 μ g/ml carbenicillin and 34 μ g/ml chloramphenicol, until the absorbance at 600nm reached a value of 0,7. The overexpression of T7gene 10 protein-His•Tag-3A4.1 fusion protein was then induced by the addition of IPTG to a final concentration of 1mM and further

incubation at 25°C with 250 RPM agitation for 3 hours. Induced cells from a 800-ml culture were pelleted by centrifugation and frozen at -70°C. The fusion protein was purified from the soluble cell fraction by affinity chromatography based on the binding of a six histidine residues sequence (His-Tag) to 5 divalent cations (Ni^{2+}) immobilized on a metal chelation Ni-NTA resin (Qiagen, Mississauga, Canada). Briefly, the pelleted cells were thawed and resuspended in Tris buffered sucrose solution (50mM Tris, 25%(w/v) sucrose) and frozen at -10 70°C for 15 minutes. Cells were incubated 15 minutes on ice in the presence of 2mg/ml lysozyme before disruption by sonication. The lysate was centrifuged at 12000 RPM for 30 minutes and Nickel charged Ni-NTA resin (QIAGEN) was added to the supernatant for an overnight incubation at 4°C, with 10015 RPM agitation. After washing the resin with a buffer consisting of 20mM Tris, 500mM NaCl, 20mM imidazole pH 7.9, the fusion 3A4.1 protein was eluted with the same buffer supplemented with 250mM imidazole. The removal of the salt and imidazole was done by dialysis against PBS at 4°C. The20 protein concentration was determined with BCA protein assay reagent kit (Perce, Rockford, IL) and adjusted to 760 $\mu\text{g}/\text{ml}$.

To evaluate whether immunization with an epitope peptide sequence could confer protection against disease, groups of 625 female CBA/N (xid) mice (National Cancer Institute) are immunized subcutaneously three times at three-week intervals with affinity purified T7gene10 protein-His-Tag-3A4.1 fusion protein or, as control, with QuilA adjuvant alone in PBS. Twelve to fourteen days following the third immunization, the30 mice are challenged intravenously with S. pneumoniae WU2 strain or intranasally with P4241 strain. Samples of the S. pneumoniae challenge inoculum are plated on chocolate agar plates to determine the number of CFU and to verify the challenge dose. The challenge dose are approximalety 300 CFU.35 Deaths are recorded daily for a period of 14 days and on day

14 post-challenge, the surviving mice are sacrificed and blood samples tested for the presence of S. pneumoniae organisms. The 3A4.1 protein or other tested protein is said protective when the number of mice surviving the infection or the median
5 number of days to death is significantly greater in the 3A4.1-immunized group compared to the control mock-immunized group.

EXAMPLE 8

10 This example illustrates the improvement of the antibody response to pneumococci using BVH-3 fragments and variants thereof.

The combined results obtained from studies of Mab reactivity
15 with truncated gene products, epitope-expressing colonies and live intact pneumococci presented in examples 2, 3 and 6, allowed to delineate between surface-exposed and internal epitopes. The epitopes detected by Mabs that efficiently bound to pneumococci cells mapped to a region comprised
20 between amino acid residues 223 to 1039 of BVH-3 described in SEQ ID NO 6. The existence of protective epitopes in the BVH-3-carboxyl half was confirmed by demonstrating that mice immunized with NEW1 molecule were protected from fatal infection with P4241 strain.

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Gene sequence comparison revealed that in some strains, the region of BVH-3 encoding for amino acids 244 to 420 as described in SEQ ID NO6 is absent thus suggesting the lack of utility of this sequence in vaccine to prevent disease caused
30 by such strains (SEQ ID NO: 9 versus SEQ ID NO: 1). Further BVH-3 fragments or variants thereof were designed in the purpose to develop a universal highly effective vaccine that would target the immune response to ubiquitous surface-exposed protective epitopes. BVH-3 gene fragments designated NEW1
35 (encoding amino acid residues 472 to 1039 from SEQ ID NO: 6) and NEW40 (encoding amino acid residues 408 to 1039 from SEQ

ID NO: 6) were amplified from the S. pneumoniae strain SP64 by PCR using pairs of oligonucleotides engineered for the amplification of the appropriate gene fragment. Each of the primers had a restriction endonuclease site at the 5' end, thereby allowing directional in-frame cloning of the amplified product into the digested plasmid vector. PCR-amplified products were digested with restriction endonucleases and ligated to linearized plasmid pET21 (Novagen) expression vector digested likewise. Oligonucleotide primers HAMJ489 (ccgaattccatatgcaaattgggcaaccgactc; NdeI) and HAMJ279 (cgccaagcttcgctatgaaatcagataaattc; HindIII) were used for the NEW 40 construction. Clones were first stabilized in E. coli DH5 α before introduction into E. coli BL21 (λ DE3) for expression of the truncated gene products. Variants from NEW1 and NEW40 were generated by mutagenesis using the Quickchange Site-Directed Mutagenesis kit from Stratagene and the oligonucleotides designed to incorporate the appropriate mutation. The presence of 6 histidine tag residues on the C-terminus of the recombinant molecules simplified the purification of the proteins by nickel chromatography. The following tables 12 and 13 describe the sequences of the primers used for the mutagenesis experiments and the variant gene products generated, respectively. Mutagenesis experiments using primer sets 39, 40, 46, 47 or 48 resulted in silent changes and were performed in the purpose of improving the expression of the desired gene or gene fragment since it was observed that during the course of expression, BVH-3 gene and fragments of, shorter secondary translation initiation products were coexpressed.

Table 12. List of PCR oligonucleotide primer sets used for site-directed mutagenesis on BVH-3 gene truncates

Primer set	Primer identification	SEQ ID No	Primer SEQUENCE 5' ---> 3'
9	HAMJ513	177	GAATCAGGTTTGTCTATGAGTTCGGAGACCACAAATCATTTATTC
	HAMJ514	178	GAAATAATGATTGTGTTCCGGAATCATGACAAACCTGATTC
10	HAMJ515	179	GTCAATGAGTTCGGAGACTCCAATCATTTATTTCTTCAAGAAGG
	HAMJ516	180	CCTTCTTGAAGAAATAATGATTGGAGTCTCCGGAATCATGAC
11	HAMJ517	181	ATGAGTTCGGAGACTCCAATTTCTTATTTCTTCAAGAAGGACTTG
	HAMJ518	182	CAAGTCTTCTTGAAGAAATAAGAAATGGAGTCTCCGGAATCAT
14	CHAN51	183	GCGATTATTTATCCGTCCTGGAGATCACCATCATGC
	CHAN52	184	GCATGATGGTGATCTCCAGACGGATAAATAATCGC
17	CHAN53	185	CCGTCCTGGAGATGGCCATCATGCAGATCCG
	CHAN54	186	CGGATCTGCATGATGGCCATCTCCAGACGG
19	CHAN47	187	CCGAGGGAGATAAGCGTTCATGCAGATCCGATTG
	CHAN48	188	CAATCGGATCTGCATGACGCTTATCTCCCTGCGG
20	CHAN55	189	CCGTCCTGGAGATGGCATCTCATGCAGATCCGATTG
	CHAN56	190	CAATCGGATCTGCATGAGTGCCATCTCCAGACGG
22	CHAN57	191	CCGTCCTGGAGATGGCATCTTCTGCAGATCCGATTGATG
	CHAN58	192	CATCAATCGGATCTGCAGAAAGTGCCATCTCCAGACGG
23	HAMJ523	193	CCGATGGAGATGGCCATCATGCAGATCCG
	HAMJ524	194	CGGATCTGCATGATGGCCATCTCCATGCGG
24	HAMJ526	195	GTCAATGATCACGGAGACTCCAATCATTTATTTCTTCAAGAAGG
	HAMJ527	196	CCTTCTTGAAGAAATAATGATTGGAGTCTCCGTGACTCATGAC
25	HAMJ528	197	ATGAGTCACGGAGACCAACAATTTCTTATTTCTTCAAGAAGGACTTG
	HAMJ529	198	CAAGTCTTCTTGAAGAAATAAGAAATGGTGGTCTCCGTGACTCAT
29	HAMJ569	199	TACCTCATTTATGACTCTTACTCTTAACATCAAAATTTGAGTGGTTTG
	HAMJ570	200	CAAAACCACTCAAAATTTGATGTTAGAGTAAGAGTCATAATGAGGTA
30	HAMJ571	201	TACCTTCTTATGACCATTACTCTAACATCAAAATTTGAGTGGTTTG
	HAMJ572	202	AAACCACTCAAAATTTGATGTTAGAGTAATGGTCAATAAGAAGGTA
31	HAMJ573	203	AACGGTAGTTTAATCATACCTTCTAAAGACCATTACCATACATC
	HAMJ574	204	GATGTTATGGTAATGGTCTTTAGAAAGGTATGATTAAACTACCGTT

Primer set	Primer identification	SEQ ID No	Primer SEQUENCE 5' ---> 3'
32	HAMJ575	205	CGGTAGTTTAAATCATACCTCATAAAGGACTCTTACCATAACATCAAA
	HAMJ576	206	TTTGATGTTATGTTAAGAGTCCTTATGAGGTATGATTAACATACCG
33	HAMJ577	207	AACGGTAGTTTAAATCATACCTGACCATTAACCATAAACATCAAAATTG
	HAMJ578	208	CAAAATTGATGTTATGTTAATGGTCAGGTATGATTAACATACCGTT
34	HAMJ579	209	AACGGTAGTTTAAATCATACCTTACCATAACATCAAAATTGAGTGG
	HAMJ580	210	CCACTCAAATTTGATGTTATGTTAAGGTATGATTAACATACCGTT
35	HAMJ581	211	ACCGTAGTTTAAATCATACCTTAACATCAAAATTGAGTGGTTGAC
	HAMJ582	212	GTCAAACCACTCAAATTTGATGTTAGGTATGATTAACATACCGTT
37	HAMJ536	213	CCTATGTAACTCCACATATAAACCCATAGCCACTGG
	HAMJ537	214	CCAGTGGCTATGGGTTATATGTGGAGTTACATAGG
39	HAMJ550	215	CGTGAAAGTATGTCGTAAATATAAGAAAAAATGCG
	HAMJ551	216	CGCATTTTCTTTTATTTTACGACAATACTTTTCAG
40	HAMJ586	217	CATGAAGAAGATGGTTACGGTTTCGATGCTAACCGTATTAATCGCTGAAG
	HAMJ587	218	CTTCAGCGATTAATACGGTTAGCATCGAAACCGTAACCATCTTCTCTG
41	HAMJ588	219	GAATCAGGTTTTGTCATGAGTGCACCAATCATTTTCTTC
	HAMJ589	220	GAAGAAATAATGATTTGTTGTCATGAGTAAATCATTTTCTCAAG
42	HAMJ590	221	GAAGATGAATCAGGTTTGTGTCATGAGTAAATCATTTTCTCAAG
	HAMJ591	222	CTTGAAGAAATAATGATTTGTCATGAGTAAATCATTTTCTCAAG
43	HAMJ592	223	GAAGATGAATCAGGTTTGTGTCATGAGTAAATCATTTTCTCAAG
	HAMJ593	224	GTCCCTTCTTGAAGAAATAATGATTTGTCATGAGTAAATCATTTTCTCAAG
44	HAMJ594	225	AAAATGCGATTATTTATCCGCAACCATCATGAGATCCGATTG
	HAMJ595	226	CAATCGGATCTGCATGATGTTGCGGATAAATAATCGCATTTT
45	HAMJ600	227	AAAATGCGATTATTTATCCGCGAGATCCGATTGATGAACATAAAC
	HAMJ601	228	GTTTATGTTTCATCAATCGGATCTGCCGGATAAATAATCGCATTTT
46	HAMJ604	229	GATGCTAACCGTATAATCGCCGAAGACGAATCAGGTTTGTGTCATG
	HAMJ605	230	CATGACAAAACCTGATTTCTGTCGCGATTATACGGTTAGCATC
47	HAMJ606	231	CGCCGAAGACGAATCCGGCTTTGTAATGATGATCAGGAGACTCC
	HAMJ607	232	GGAGTCTCCGTGACTCATTAACAAAGCCGGATTCTGTTCCGGCG
48	HAMJ608	233	CATCTCATGAACAGGATTATCCCGGCAACGCCAAAGAAATGAAAG
	HAMJ609	234	CTTTTCATTTCTTTGGCGTTGCCGGGATAATCCTGTTCAATGAGATG

Table 13. Lists of truncated variant BVH-3 gene products generated from *S. pneumoniae* SP64

Protein designation	Gene/ Protein SEQ ID NO	Protein Identification*	PCR primer set (ref. table 12)	Gene used for mutagenesis
NEW1- mut1**	255	NEW1	39	NEW1
NEW35A	256	NEW1 550-SGDGTS-555	14, 17, 20, 22	NEW1
NEW42	257	NEW40 55-SGDSNS-60 144-SGDGTS-149	9, 10, 11, 14, 17, 20, 22	NEW40
NEW49	258	NEW40 55-SGDHNH-60	9	NEW40
NEW50	259	NEW40 55-SGDSNH-60	10	NEW49
NEW51	260	NEW40 55-SGDHNH-60 144-SGDHHH-149	14	NEW49
NEW52	261	NEW40 55-SGDSNH-60 144-SGDGHH-149	10, 17	NEW51
NEW53	262	NEW40 55-HGDHNH-60 144-SGDHHH-149	14	NEW40
NEW54	263	NEW40 55-SGDHNH-60 144-SGDGHH-149	17	NEW53
NEW55	264	NEW1 550-HGDGHH-555	23	NEW1
NEW56	265	NEW40 55-HGDSNH-60 144-SGDHHH-149	24	NEW53
NEW56- mut2**	266	NEW56	40	NEW56
NEW56- mut3**	267	NEW56	46, 47, 48	NEW56
NEW57	268	NEW40 55-HGDHNS-60 144-SGDHHH-149	25	NEW53
NEW63	269	NEW40 55-HGDSNH-60 144-HGDHHH-149	24	NEW40
NEW64	270	NEW40 55-HGDHNS-60 144-HGDHHH-149	25	NEW40
NEW65	271	NEW40 55-HGDSNH-60 144-HGDGHH-149	23	NEW63

Protein designation	Gene/ Protein SEQ ID NO	Protein Identification*	PCR primer set (ref. table 12)	Gene used mutagenesis	for
NEW66	272	NEW40 55-HGDHNS-60 144-HGDGHH-149	23	NEW64	
NEW76	273	NEW40 55-HGDHNS-60 144-SGDGHH-149	17	NEW64	
NEW105	274	NEW40 55-____-60	41, 42, 43	NEW40	
NEW106	275	NEW40 144-____-149	44, 45	NEW40	
NEW107	276	NEW40 55-____-60 144-____-149	44, 45	NEW105	

* The underlined amino acid residues represent the modification in protein sequence. Nucleotides/amino acid residues are deleted in NEW105, NEW106 and NEW107 constructs.

** silent mutation, i.e. the polypeptide is the same as New1.

Groups of 7 or 8 female BALB/c mice (Charles River) immunized as described earlier in example 1 were used for protection experiments against intranasal challenge with virulent S. pneumoniae P4241 strain. The mice were observed for 10 to 14 days post-infection. Data from Table 15 clearly indicate that the NEW35A molecule was equivalent to the parental NEW1 in term of protection. Interestingly, high survival rates were obtained for NEW40- and NEW56-immunized groups with 7 and 8 survivors out of 8 animals, respectively. Similarly, NEW25 comprising amino acid residues 233 to 1039 protected 7 out of 8 animals from lethal infection.

Table 14. Protection mediated by BVH-3 fragments or variants thereof in experimental pneumonia

Experiment	Immunogen	Alive : Dead	Days to death post-infection
1	Quil A	0 : 8	4, 4, 4, 4, 4, 4, 4, 4
	NEW 1	5 : 3	5, 7, 7, >14, >14, >14, >14, >14
	NEW 35A	5 : 2	9, 10, >14, >14, >14, >14, >14
	NEW 40	7 : 1	13, >14, >14, >14, >14, >14, >14, >14
	BVH-3M	4 : 4	7, 8, 10, 12, >14, >14, >14, >14
2	Quil A	0 : 8	3, 3, 4, 4, 4, 4, 4, 4
	NEW 52	4 : 4	7, 7, 8, 9, >10, >10, >10, >10
	NEW56	8 : 0	8 X >10
	NEW 40	7 : 1	6, >10, >10, >10, >10, >10, >10, >10
3	QuilA	0 : 8	3, 3, 4, 4, 4, 4, 4, 4
	NEW25	7 : 1	6, >13, >13, >13, >13, >13, >13, >13

Additionally, flow cytometry analyses of the binding capacity of the sera antibodies from the vaccinated animals revealed that NEW40 and NEW56 antibodies labelled live intact pneumococci more efficiently than antibodies raised to BVH-3M (Table 15).

Table 15. Binding of mouse sera antibodies at the surface of S. pneumoniae type 3 strain WU2 as measured by flow cytometry.

Antisera	Fluorescence index			
	Experiment 1	Experiment 2	Experiment 3	Mean \pm SE
BVH-3M	9.2	11.4	14.5	11.7 \pm 1.5
NEW1	11.5	10.1	nd*	10.8 \pm 0.7
NEW35A	14.3	12.9	nd	13.6 \pm 0.7
NEW40	20.4	19.1	20.2	19.9 \pm 0.4
NEW56	nd	16.7	20.2	18.5 \pm 1.8
NEW52	nd	16.6	19.3	18.0 \pm 1.4
Adjuvant alone	1.9	1.6	1.2	1.6 \pm 0.2

* nd: not done

5 Cytometry results are expressed as fluorescence index value where the fluorescence index is the median fluorescence value of pneumococci treated with test sera divided by the background fluorescence value of pneumococci treated with the fluorescein conjugate alone. In these flow cytometric assays,
10 all sera were used at a dilution of 1 :50 and the sera from mice immunized with BVH-3C fragment or QuilA adjuvant alone gave a value similar to the background value.

15 Altogether the protection and pneumococci antibody binding data indicate that vaccination using NEW1 or NEW40 molecules and variants thereof, directs the immune response to conserved protective surface-exposed epitopes.

EXAMPLE 9

20 This example describes the cloning and expression of a chimeric deletant BVH-11-2 gene encoding for a chimeric polypeptide corresponding to BVH-11-2 conserved protective surface-exposed epitopes present in most if not all S. pneumoniae strains.

BVH-11-2 gene fragments corresponding to 4 gene regions, were amplified by PCR using pairs of oligonucleotides engineered to amplify fragments originating from SEQ ID NO :5 spanning nucleotides 1662 to 1742, 1806 to 2153, 2193 to 2414 and 2484 to 2627 from S. pneumoniae strain Sp64 BVH-11-2 gene.

The primers used, HAMJ490-491, HAMJ492-HAMJ493, HAMJ494-HAMJ495, HAMJ496-HAMJ354 had a restriction endonuclease site at the 5' end, thereby allowing directional in-frame cloning of the amplified product into the digested pET21b(+) plasmid vector (Table 16). PCR-amplified products were digested with restriction endonucleases and ligated to linearized plasmid pSL301 vector digested likewise except for the PCR-amplified fragment obtained with the primer pair HAMJ490-HAMJ491. The HAMJ490-HAMJ491 PCR-amplified product was purified from agarose gel using a QIAquick gel extraction kit from QIAGEN (Chatsworth, CA) and ligated into pGEM-T plasmid vector without any prior restriction endonuclease digestion. The resultant plasmid constructs were confirmed by nucleotide sequence analysis. The recombinant plasmids containing each of the four were digested with restriction endonucleases corresponding with the 5' end of each primer pair used for the PCR-amplification. The fragments were purified from agarose gel like described earlier and were all ligated to linearized plasmid pET21b (+) digested with the restriction enzymes NdeI and HindIII for the in-frame cloning of the four different regions of the BVH11-2 gene. Clones were first stabilized in E.coli DH5 α before introduction into E.coli BL21 (λ DE3) for expression of a chimeric pneumococcal protein molecule..

The resulting NEW43 gene sequence (SEQ ID No 257) is described in Figure 33.

The deduced amino acid sequence of NEW43 protein (SEQ ID No 258) is described in Figure 34.

Table 16. List of PCR oligonucleotide primers used to construct the NEW43 , VP43S and NEW86

Primer	SEQ ID NO	Sequence 5' - 3'	Nucleotide position	Restriction sites
HAMJ490	259	ccgaattccatattgcaaattacctacactgatgatg	SEQ ID 5 :1662-1683	NdeI
HAMJ491	260	ggactagtagtcaaagatat aaccgtcttc	SEQ ID 5 :1742-1722	SpeI
HAMJ492	261	ggactagttggattaaaaa agatagtttgtctg	SEQ ID 5 :1806-1830	SpeI
HAMJ493	262	ttcccgcgggttcgacatag tacttgacagtcg	SEQ ID 5 :2153-2131	SacII
HAMJ494	263	ttcccgcggaacgctagtg accatgttcg	SEQ ID 5 :2193-2212	SacII
HAMJ495	264	cggggtaccaggaatttca gcctcatctgtg	SEQ ID 5 :2414-2393	KpnI
HAMJ496	265	cccgggtacccttagtatta gacaaaatgctatggag	SEQ ID 5 :2484-2510	KpnI
HAMJ 354	65	cgccaagcttctgtatagg agccggttgac	SEQ ID 5 :2627-2608	HindIII
HAMJ 583	266	ggatcccgggaggtatgat taaactaccg	SEQ ID 5 :2039-2021	SmaI
HAMJ 584	267	catgcccgggaacatcaaa tttgagtgggttgac	SEQ ID 5 :2058-2081	SmaI
HAMJ 610	268	cttgatcgacatatgttgg caggcaagtacacaacag	SEQ ID 5 :1701-1722	NdeI

Table 17. List of truncated BVH-11-2 gene fragments generated from *S. pneumoniae* SP64 for the construction of NEW43

PCR-primer sets	Gene fragment designation	Corresponding amino acid residues on SEQ ID NO: 8	Cloning vector
HAMJ490-HAMJ491	NEW43a	517-543	pGEM-T
HAMJ492-HAMJ493	NEW43b	565-680	pSL301
HAMJ494-HAMJ495	NEW43c	694-767	pSL301
HAMJ496-HAMJ354	NEW43d	791-838	pSL301

5

Table 18. Properties of NEW86 and VP43S genes generated from NEW43 gene

PCR-primer sets	Gene/ Protein designation	Identification
HAMJ610-HAMJ354	VP43S	NEW43 C'end corresponding to residues 15-272)
HAMJ490-HAMJ583 HAMJ584-HAMJ354	NEW86	NEW43 109-__PG__-114

10 NEW43-derived molecules designated VP43S and NEW86 were generated from gene amplification and cloning experiments using PCR primers described in Tables 16 and 18 and pET21 expression plasmid vector. Variants from NEW43 were generated by mutagenesis using the Quickchange Site-Directed Mutagenesis
 15 kit from Stratagene and the oligonucleotides designed to incorporate the appropriate mutation. The presence of 6 histidine tag residues on the C-terminus of the recombinant molecules simplified the purification of the proteins by nickel chromatography. The following tables 19 and 20
 20 describe the sequences of the primers used for the mutagenesis experiments and the NEW43 variant gene products generated, respectively.

5 Table 19. List of PCR oligonucleotide primer sets used for site-directed mutagenesis on NEW43 gene

Primer set	Primer identification	SEQ ID NO	Primer SEQUENCE 5' ---> 3'
1	HAMJ 497	269	AACGGTAGTTTAATCATACCTTCTTATGACCATTACCATAACATC GATGTTATGGTAATGGTCATAAGAAGGTATGATTAAACTACCGTT
	HAMJ 498	270	
2	HAMJ499	271	AATCATACCTTCTTATGACTCTTACCATAACATCAAATTTGAGTG CACTCAAATTTGATGTTATGGTAAGAGTCATAAGAAGGTATGATT
	HAMJ500	272	
3	HAMJ501	273	TACCTTCTTATGACTCTTACTCTAACATCAAATTTGAGTGGTTTG CAAACCACTCAAATTTGATGTTAGAGTAAGAGTCATAAGAAGGTA
	HAMJ502	274	
26	HAMJ530	275	AATCATACCTCATTATGACTCTTACCATAACATCAAATTTGAGTG CACTCAAATTTGATGTTATGGTAAGAGTCATAATGAGGTATGATT
	HAMJ531	276	
27	HAMJ532	277	TACCTCATTATGACCATTACTCTAACATCAAATTTGAGTGGTTTG CAAACCACTCAAATTTGATGTTAGAGTAATGGTCATAATGAGGTA
	HAMJ533	278	
29	HAMJ569	279	TACCTCATTATGACTCTTACTCTAACATCAAATTTGAGTGGTTTG CAAACCACTCAAATTTGATGTTAGAGTAAGAGTCATAATGAGGTA
	HAMJ570	280	
30	HAMJ571	281	TACCTTCTTATGACCATTACTCTAACATCAAATTTGAGTGGTTTG AAACCACTCAAATTTGATGTTAGAGTAATGGTCATAAGAAGGTA
	HAMJ572	282	
31	HAMJ573	283	AACGGTAGTTTAATCATACCTTCTAAAGACCATTACCATAACATC GATGTTATGGTAATGGTCTTTAGAAGGTATGATTAAACTACCGTT
	HAMJ574	284	
32	HAMJ575	285	CGGTAGTTTAATCATACCTCATAAGGACTCTTACCATAACATCAAA TTGATGTTATGGTAAGAGTCCTTATGAGGTATGATTAAACTACCG
	HAMJ576	286	
33	HAMJ577	287	AACGGTAGTTTAATCATACCTGACCATTACCATAACATCAAATTTG CAAATTTGATGTTATGGTAATGGTCAGGTATGATTAAACTACCGTT
	HAMJ578	288	
34	HAMJ579	289	AACGGTAGTTTAATCATACCTTACCATAACATCAAATTTGAGTGG CCACTCAAATTTGATGTTATGGTAAGGTATGATTAAACTACCGTT
	HAMJ580	290	
35	HAMJ581	291	ACCGGTAGTTTAATCATACCTAACATCAAATTTGAGTGGTTTGAC GTCAAACCACTCAAATTTGATGTTAGGTATGATTAAACTACCGTT
	HAMJ582	292	

Table 20. List of NEW43 variant gene products generated from *S. pneumoniae* SP64

Polypeptide designation	Polypeptide SEQ ID NO	Polypeptide identification*	PCR primer set (ref. table 22)	Gene used for mutagenesis
NEW60	293	NEW43 109- <u>SYD</u> HYH-114	1	NEW43
NEW61	294	NEW43 109-HYD <u>SYH</u> -114	26	NEW43
NEW62	295	NEW43 109-HYD <u>HYS</u> -114	27	NEW43
NEW80	296	NEW43 109- <u>SYD</u> <u>SYH</u> -114	2	NEW60
NEW81	297	NEW43 109- <u>SYD</u> <u>SYS</u> -114	3	NEW80
NEW82	298	NEW43 109-HYD <u>SYS</u> -114	29	NEW61
NEW83	299	NEW43 109- <u>SYD</u> <u>HYS</u> -114	30	NEW60
NEW84	300	NEW43 109- <u>SKD</u> HYH-114	31	NEW60
NEW85	301	NEW43 109-H <u>KD</u> SYH-114	32	NEW61
NEW88D1	302	NEW43 109-__ <u>D</u> HYH-114	33	NEW43
NEW88D2	303	NEW43 109-____ <u>YH</u> -114	34	NEW88D1
NEW88	304	NEW43 109-_____-114	35	NEW88D2

* The underlined amino acid residues represent the modification in protein sequence. Nucleotides/amino acid residues are deleted in NEW88D1, NEW88D2 and NEW88 constructs.

Groups of 7 or 8 female BALB/c mice (Charles River) immunized as described earlier in example 1 were used for protection experiments against intranasal challenge with virulent *S. pneumoniae* P4241 strain. Data from Table 21 clearly indicate that NEW 19, NEW43 and variants thereof provided protection against experimental pneumonia.

Table 21. Protection mediated by NEW19 and NEW43 fragments or variants thereof in experimental pneumonia

Experiment	Immunogen	Alive : Dead	Median day alive
1	Quil A	0 : 8	4, 4, 4, 4, 4, 4, 4, 5
	NEW 19	7 : 1	5, 7X >14
	NEW 43	8 : 0	8X >14
2	Quil A	0 : 8	4, 4, 4, 4, 4, 5, 5, 5
	NEW 43	7 : 1	8, 7X >14
	NEW 80	6 : 2	5, 6, 6 X >14
	NEW 83	6 : 2	8, 10, 6 X >14
3	Quil A	0 : 8	4, 4, 4, 4, 5, 5, 5, 5
	NEW 43	7 : 1	5, 7X >8
	NEW 88D1	5 : 3	5, 6, 6, 6 X >8
	NEW 88D2	5 : 3	6, 6, 6, 6 X >8
	NEW 88	7 : 1	6, 7X >8
3	Quil A	0 : 8	4, 4, 4, 5, 5, 5, 5, 6
	NEW 60	8 : 0	8 X >8
	NEW 84	8 : 0	8 X >8
	NEW 85	5 : 3	5, 7, 7, 5 X >8
	NEW 86	5 : 3	5, 6, 6, 5 X >8

5

EXAMPLE 10

This example describes the cloning and expression of chimeric genes encoding for a chimeric protein corresponding to the carboxy-terminal region of BVH-3 or variants thereof in fusion, at either the carboxyl end or the amino end, to NEW43 or variants thereof.

The chimeric genes comprising a BVH-3 truncate variant gene and a NEW43 or NEW43 variant gene have been designed following

the procedure described in example 1. The polypeptides encoded by these chimeric genes are listed in the table 22. Briefly, gene fragments to be included in a chimeric gene were amplified by PCR using pairs of oligonucleotides engineered so that the primers had a restriction endonuclease site at the 5' end, thereby allowing directional in-frame cloning of the amplified product into digested plasmid vectors (Table 23 and Table 24). PCR-amplified products were digested with restriction endonucleases and ligated to linearized plasmid pSL301 vector. The resultant plasmid construct were confirmed by nucleotide sequence analysis. The recombinant pSL301 plasmids containing a PCR product were redigested with the same endonuclease restriction enzyme for the obtention of the DNA inserts. The resulting insert DNA fragments were purified and inserts corresponding to a given chimeric gene were ligated into pURV22-NdeI vector for the generation of a chimeric gene. The expressed recombinant proteins were purified from supernatant fractions obtained from centrifugation of sonicated heat-induced E. coli cultures using multiple chromatographic purification steps.

Table 22. List of polypeptides encoded by chimeric genes comprising a BVH-3 truncate variant gene and a NEW43 or NEW43 variant gene

Polypeptide designation	SEQ ID NO	Identification
VP 89	327	M-New56 -GP- New43*
VP 90	328	M-New43 -GP- New56
VP 91	329	M-New52 -GP- New43
VP 92	330	M-New43 -GP- New52
VP 93	331	M-New56 -GP- New60
VP 94	332	M-New60 -GP- New56
VP 108	333	M-New56 -GP- New88
VP109	334	M-New88 -GP- New56

Polypeptide designation	SEQ ID NO	Identification
VP 110	335	M-New60 -GP- New105
VP 111	336	M-New60 -GP- New107
VP112	337	M-New88 -GP- New105
VP113	338	M-New88 -GP- New107
VP114	339	M-New80-GP- New105
VP115	340	M-New80 -GP- New107
VP116	341	M-New83 -GP- New105
VP117	342	M-New83 -GP- New107
VP119	343	M-New43S- GP-New105
VP120	344	M-New43S- GP-New107
VP121	345	M-New80S- GP-New105
VP122	346	M-New80S- GP-New107
VP123	347	M-New88S- GP-New105
VP124	348	M-New88S- GP-New107

* Encoded amino acids for the chimeras are expressed as the gene product, additional amino acid residues were added. M is methionine, G is glycine and P is proline.

Table 23. List of PCR oligonucleotide primer pairs designed for the generation of the chimeric genes encoding the polypeptides listed in Table 22.

Primer set	PCR-primer identification	Gene used for PCR amplification	Corresponding position of the gene fragment on
49	HAMJ490-HAMJ471	Variant New43	N-terminal
50	HAMJ564-HAMJ556	Variant New43	C-terminal
51	HAMJ489-HAMJ359	Variant New40	N-terminal
52	HAMJ559-HAMJ557	Variant New40	C-terminal
53	HAMJ610-HAMJ471	Variant New43S	N-terminal

5 Table 24. List of PCR oligonucleotide primers designed for the generation of the chimeric genes encoding the polypeptides listed in Table 22.

Primer	SEQ ID NO	Sequence 5' - 3'	Restriction site
HAMJ490	259	ccgaattccatatgcaaattaccta cactgatgatg	NdeI
HAMJ471	168	atatggggcccctgtataggagccgg ttgactttc	ApaI
HAMJ564	327	atatggggcccaaattacctacact gatgatgagattcagg	ApaI
HAMJ556	328	ataagaatgcggccgcctactgtat aggagccggttgactttc	NotI
HAMJ489	329	ccgaattccatatgcaaattgggca accgactc	NdeI
HAMJ359	173	tcccggggccccgctatgaaatcaga taaattc	ApaI
HAMJ559	330	atatggggcccaaattgggcaaccg actc	ApaI
HAMJ354	65	cgccaagcttctgtataggagccgg ttgac	HindIII
HAMJ610	268	cttgatcgacatatgttggcaggca agtacacaacag	NdeI
HAMJ557	331	ataagaatgcggccgcttacgctat gaaatcagataaattc	NotI
HAMJ279	35	cgccaagcttcgctatgaaatcaga taaattc	HindIII

What is claimed is:

1. An isolated polynucleotide comprising a polynucleotide chosen from;
 - (a) a polynucleotide encoding a polypeptide having at least 70% identity to a second polypeptide chosen from: table B, E or H;
 - (b) a polynucleotide encoding a polypeptide having at least 95% identity to a second polypeptide chosen from: table B, E or H;
 - (c) a polynucleotide encoding a polypeptide having an amino sequence chosen from table B, E or H or fragments, analogs or derivatives thereof;
 - (d) a polynucleotide encoding a polypeptide chosen from: table B, E or H;
 - (e) a polynucleotide encoding a polypeptide capable of generating antibodies having binding specificity for a polypeptide having a sequence chosen from: table B, E or H,
 - (f) a polynucleotide encoding an epitope bearing portion of a polypeptide chosen from table B, E or H; and
 - (g) a polynucleotide complementary to a polynucleotide in (a), (b), (c), (d), (e) or (f).
2. The isolated polynucleotide of claim 1 wherein said polynucleotide is (a).
3. The isolated polynucleotide of claim 1 wherein said polynucleotide is (b).
4. The isolated polynucleotide of claim 1 wherein said polynucleotide is (c).
5. The isolated polynucleotide of claim 1 wherein said polynucleotide is (d).
6. The isolated polynucleotide of claim 1 wherein said polynucleotide is (e).

7. The isolated polynucleotide of claim 1 wherein said polynucleotide is (f).
8. The isolated polynucleotide of claim 1 wherein said polynucleotide is (g).
9. The isolated polynucleotide of claim 7 wherein said polynucleotide is chosen from table B.
10. The isolated polynucleotide of claim 9 wherein said epitope bearing portion is chosen from table C.
11. The isolated polynucleotide of claim 7 wherein said polynucleotide is chosen from table E.
12. The isolated polynucleotide of claim 11 wherein said epitope bearing portion is chosen from table F.
13. The polynucleotide of anyone of claims 1 to 12, wherein said polynucleotide is DNA.
14. The polynucleotide of anyone of claims 1 to 12, wherein said polynucleotide is RNA.
15. A vector comprising the polynucleotide of claim 13, wherein said DNA is operably linked to an expression control region.
16. A host cell transfected with the vector of claim 15.
17. A process for producing a polypeptide comprising culturing a host cell according to claim 16 under conditions suitable for expression of said polypeptide.
18. An isolated polypeptide comprising a member chosen from:

- (a) a polypeptide having at least 70% identity to a second polypeptide having an amino acid sequence chosen from: table B, E or H;
 - (b) a polypeptide having at least 95% identity to a second polypeptide having an amino acid sequence chosen from: table B, E or H;
 - (c) a polypeptide having an amino acid sequence chosen from table B, E or H;
 - (d) a polypeptide having amino acid sequence chosen from: table B, E or H or fragments, analogs or derivatives thereof;
 - (e) a polypeptide capable of generating antibodies having binding specificity for a second polypeptide having a sequence chosen from table B, E or H;
 - (f) an epitope bearing portion of a polypeptide having an amino acid sequence chosen from: table B, E or H;
 - (g) the polypeptide of (a), (b), (c), (d), (e), or (f) wherein wherein the N-terminal Met residue is deleted; or
 - (h) the polypeptide of (a), (b), (c), (d), (e), or (f) wherein the secretory amino acid sequence is deleted.
19. The polypeptide of claim 18 wherein said polypeptide is (f).
20. The polypeptide of claim 19 wherein said is chosen from table B.
21. The polypeptide of claim 20 wherein said epitope bearing portion is chosen from table C.
22. The polypeptide of claim 19 wherein said is chosen from table E.
23. The polypeptide of claim 22 wherein said epitope bearing portion is chosen from table F.

24. A chimeric polypeptide comprising two or more polypeptides chosen from table B, E or H thereof; provided that the polypeptides are linked as to form a chimeric polypeptide.
25. A vaccine composition comprising a polypeptide according to any one of claims 18 to 24 and a pharmaceutically acceptable carrier, diluent or adjuvant.
26. A method for therapeutic or prophylactic treatment of meningitis, otitis media, bacteremia or pneumonia infection in an individual susceptible to meningitis, otitis media, bacteremia or pneumonia infection comprising administering to said individual a therapeutic or prophylactic amount of a composition according to claim 25.
27. A method for therapeutic or prophylactic treatment of streptococcal bacterial infection in an individual susceptible to streptococcal infection comprising administering to said individual a therapeutic or prophylactic amount of a composition according to claim 25.
28. A method according to claim 26, wherein said individual is a mammal.
29. A method according to claim 27, wherein said individual is a mammal
30. A method according to claim 26, wherein said individual is a human.
31. A method according to claim 27, wherein said individual is a human
32. A method according to claim 27, wherein said bacterial infection is S.pneumoniae, group A streptococcus

(*pyogenes*), group B streptococcus (GBS or *agalactiae*), *dysgalactiae*, *uberis*, *nocardia* or *Staphylococcus aureus*.

33. A method according to claim 27, wherein said bacterial infection is *S.pneumoniae*.

34. Use of a vaccine composition according to claim 25 for the prophylactic or therapeutic treatment of Streptococcal infection in an animal susceptible to or infected with streptococcal infection comprising administering to said animal a prophylactic or therapeutic amount of the composition.

ATGAAATTTA	GTAAAAATA	TATAGCAGCT	GGATCAGCTG	TTATCGTATC	CTTGAGTCTA	60
TGTGCCTATG	CACTAAACCA	GCATCGTTCG	CAGGAAAATA	AGGACAATAA	TCGTGTCTCT	120
TATGTGGATG	GCAGCCAGTC	AAGTCAGAAA	AGTGAAAAC	TGACACCAGA	CCAGGTTAGC	180
CAGAAAGAAG	GAATTCAGGC	TGAGCAAAT	GTAATCAAAA	TTACAGATCA	GGGCTATGTA	240
ACGTCACACG	GTGACCACTA	TCATTACTAT	AATGGGAAAG	TTCCTTATGA	TGCCCTCTTT	300
AGTGAAGAAC	TCTTGATGAA	GGATCCAAAC	TATCAACTTA	AAGACGCTGA	TATTGTCAAT	360
GAAGTCAAGG	GTGGTTATAT	CATCAAGGTC	GATGGAAAAT	ATTATGTCTA	CCTGAAAGAT	420
GCAGCTCATG	CTGATAATGT	TCGAACTAAA	GATGAAATCA	ATCGTCAAAA	ACAAGAACAT	480
GTCAAAGATA	ATGAGAAGGT	TAACCTAAT	GTTGCTGTAG	CAAGGTCTCA	GGGACGATAT	540
ACGACAAATG	ATGGTTATGT	CTTTAATCCA	GCTGATATTA	TCGAAGATAC	GGGTAATGCT	600
TATATCGTTC	CTCATGGAGG	TCACTATCAC	TACATTCCCA	AAAGCGATTT	ATCTGCTAGT	660
GAATTAGCAG	CAGCTAAAGC	ACATCTGGCT	GGAAAAATA	TGCAACCGAG	TCAGTTAAGC	720
TATTCTTCAA	CAGCTAGTGA	CAATAACACG	CAATCTGTAG	CAAAAGGATC	AACTAGCAAG	780
CCAGCAAATA	AATCTGAAAA	TCTCCAGAGT	CTTTTGAAGG	AACTCTATGA	TTACCTTAGC	840
GCCCAACGTT	ACAGTGAATC	AGATGGCCTG	GTCTTTGACC	CTGCTAAGAT	TATCAGTCGT	900
ACACCAAATG	GAGTTGCGAT	TCCGCATGGC	GACCATTACC	ACTTTATTCC	TTACAGCAAG	960
CTTCTGCTT	TAGAAGAAAA	GATTGCCAGA	ATGGTGCCTA	TCAGTGGAAC	TGGTTCTACA	1020
GTTTCTACAA	ATGCAAAACC	TAATGAAGTA	GTGCTTAGTC	TAGGCAGTCT	TTCAAGCAAT	1080
CCTTCTCTT	TAACGACAAG	TAAGGAGCTC	TCTTCAGCAT	CTGATGGTTA	TATTTTTAAT	1140
CCAAAAGATA	TCGTTGAAGA	AACGGCTACA	GCTTATATTG	TAAGACATGG	TGATCATTTT	1200
CATTACATTC	CAAAATCAAA	TCAAATTGGG	CAACCGACTC	TTCCAAACAA	TAGTCTAGCA	1260
ACACCTTCTC	CATCTCTTCC	AATCAATCCA	GGAAC TTCAC	ATGAGAAACA	TGAAGAAGAT	1320
GGATACGGAT	TTGATGCTAA	TCGTATTATC	GCTGAAGATG	AATCAGGTTT	TGTCATGAGT	1380
CACGGAGACC	ACAATCATTA	TTTCTTCAAG	AAGGACTTGA	CAGAAGAGCA	AATTAAGGCT	1440
GCGCAAAAC	ATTTAGAGGA	AGTTAAACT	AGTCATAATG	GATTAGATTTC	TTTGTCTATCT	1500
CATGAACAGG	ATTATCCAGG	TAATGCCAAA	GAAATGAAAG	ATTTAGATAA	AAAAATCGAA	1560
GAAAAAATG	CTGGCATTAT	GAAACAATAT	GGTGTCAAAC	GTGAAAGTAT	TGTCGTGAAT	1620
AAAGAAAAAA	ATGCGATTAT	TTATCCGCAT	GGAGATCACC	ATCATGCAGA	TCCGATTGAT	1680
GAACATAAAC	CGGTTGGAAT	TGGTCATTCT	CACAGTAACT	ATGAACTGTT	TAAACCCGAA	1740
GAAGGAGTTG	CTAAAAAGA	AGGGAATAAA	GTTTATACTG	GAGAAGAATT	AACGAATGTT	1800
GTTAATTTGT	TAAAAAATAG	TACGTTTAAT	AATCAAAACT	TTACTCTAGC	CAATGGTCAA	1860
AAACGCGTTT	CTTTTAGTTT	TCCGCCTGAA	TTGGAGAAAA	AATTAGGTAT	CAATATGCTA	1920
GTAAATTTAA	TAACACCAGA	TGGAAAAGTA	TTGGAGAAAG	TATCTGGTAA	AGTATTTGGA	1980
GAAGGAGTAG	GGAATATTGC	AAACTTTGAA	TTAGATCAAC	CTTATTTACC	AGGACAAACA	2040
TTTAAGTATA	CTATCGCTTC	AAAAGATTAT	CCAGAAGTAA	GTTATGATGG	TACATTTACA	2100
GTTCCAACCT	CTTTAGCTTA	CAAAATGGCC	AGTCAAACGA	TTTTCTATCC	TTTCCATGCA	2160
GGGGATACTT	ATTTAAGAGT	GAACCTCAA	TTTGCAGTGC	CTAAAGGAAC	TGATGCTTTA	2220
GTCAGAGTGT	TTGATGAATT	TCATGGAAAT	GCTTATTTAG	AAAATAACTA	TAAAGTTGGT	2280
GAAATCAAAT	TACCGATTCC	GAAATTAAAC	CAAGGAACAA	CCAGAACGGC	CGGAAATAAA	2340
ATTCTGTAA	CCTTCATGGC	AAATGCTTAT	TTGGACAATC	AATCGACTTA	TATTGTGGAA	2400
GTACCTATCT	TGGAAAAAGA	AAATCAAAC	GATAAACCAA	GTATTCTACC	ACAATTTAAA	2460
AGGAATAAAG	CACAAGAAAA	CTCAAAC	GATGAAAAGG	TAGAAGAACC	AAAGACTAGT	2520
GAGAAGGTAG	AAAAAGAAAA	ACTTTCTGAA	ACTGGGAATA	GTACTAGTAA	TTCAACGTTA	2580
GAAGAAGTTC	CTACAGTGGA	TCCTGTACAA	GAAAAAGTAG	CAAAATTTGC	TGAAAGTTAT	2640
GGGATGAAGC	TAGAAAATGT	CTTGTTTAAT	ATGGACGGAA	CAATTGAATT	ATATTTACCA	2700

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TCAGGAGAAG	TCATTAAAAA	GAATATGGCA	GATTTTACAG	GAGAAGCACC	TCAAGGAAAT	2760
GGTGAAAATA	AACCATCTGA	AAATGGAAAA	GTATCTACTG	GAACAGTTGA	GAACCAACCA	2820
ACAGAAAATA	AACCAGCAGA	TTCTTTACCA	GAGGCACCAA	ACGAAAAACC	TGTAAAACCA	2880
GAAAACTCAA	CGGATAATGG	AATGTTGAAT	CCAGAAGGGA	ATGTGGGGAG	TGACCCTATG	2940
TTAGATCCAG	CATTAGAGGA	AGCTCCAGCA	GTAGATCCTG	TACAAGAAAA	ATTAGAAAAA	3000
TTTACAGCTA	GTTACGGATT	AGGCTTAGAT	AGTGTATAT	TCAATATGGA	TGGAACGATT	3060
GAATTAAGAT	TGCCAAGTGG	AGAAGTGATA	AAAAAGAATT	TATCTGATTT	CATAGCGTAA	3120

(SEQ ID NO: 1)

FIGURE 1

AATTCCTTGT	CGGGTAAGTT	CCGACCCGCA	CGAAAGGCGT	AATGATTTGG	GCACTGTCTC	60
AACGAGAGAC	TCGGTGAAAT	TTTAGTACCT	GTGAAGATGC	AGGTACCCG	CGACAGGACG	120
GAAAGACCCC	ATGGAGCTTT	ACTGCAGTTT	GATATTGAGT	GTCTGTACCA	CATGTACAGG	180
ATAGGTAGGA	GTCTAAGAGA	TCGGGACGCC	AGTTTCGAAG	GAGACGCTGT	TGGGATACTA	240
CCCTTGTTGT	ATGGCCACTC	TAACCCAGAT	AGGTGATCCC	TATCGGAGAC	AGTGTCTGAC	300
GGGCAGTTTG	ACTGGGGCGG	TCGCCTCCTA	AAAGGTAACG	GAGGCGCCCA	AAGGTTCCCT	360
CAGAATGGTT	GGAAATCATT	CGCAGAGTGT	AAAGGTATAA	GGGAGCTTGA	CTGCGAGAGC	420
TACAACTCGA	GCAGGGACGA	AAGTCGGGCT	TAGTGATCCG	GTGGTTCCGT	ATGGAAGGGC	480
CATCGCTCAA	CGGATAAAAG	CTACCCTGGG	GATAACAGGC	TTATCTCCCC	CAAGAGTTCA	540
CATCGACGGG	GAGGTTTGGC	ACCTCGATGT	CGGCTCGTCG	CATCCTGGGG	CTGTAGTCGG	600
TCCCAAGGGT	TGGGCTGTTC	GCCCATTAAG	GCGGCACGCG	AGCTGGGTTC	AGAACGTCGT	660
GAGACAGTTC	GGTCCCTATC	CGTCGCGGGC	GTAGGAAATT	TGAGAGGATC	TGCTCCTAGT	720
ACGAGAGGAC	CAGAGTGGAC	TTACCGCTGG	TGTACCAGTT	GTCTTGCCAA	AGGCATCGCT	780
GGGTAGCTAT	GTAGGGAAGG	GATAAACGCT	GAAAGCATCT	AAGTGTGAAA	CCCACCTCAA	840
GATGAGATTT	CCCATGATTA	TATATCAGTA	AGAGCCCTGA	GAGATGATCA	GGTAGATAGG	900
TTAGAAAGTG	AAGTGTGGCG	ACACATGTAG	CGGACTAATA	CTAATAGCTC	GAGGACTTAT	960
CCAAAGTAAC	TGAGAATATG	AAAGCGAACG	GTTTCTTAA	ATTGAATAGA	TATTCAATTT	1020
TGAGTAGGTA	TTACTCAGAG	TTAAGTGACG	ATAGCCTAGG	AGATACACCT	GTACCCATGC	1080
CGAACACAGA	AGTTAAGCCC	TAGAACGCCG	GAAGTAGTTG	GGGGTTGCCC	CCTGTGAGAT	1140
AGGGAAGTCG	CTTAGCTCTA	GGGAGTTTAG	CTCAGCTGGG	AGAGCATCTG	CCTTACAAGC	1200
AGAGGGTCAG	CGGTTTCGATC	CCGTTAATCT	CCAAAGGTCC	CGTAGTGTAG	CGGTTATCAC	1260
GTCGCCCTGT	CACGGCGAAG	ATCGCGGGTT	CGATTCCCGT	CGGGACCGTT	TAAGGTAACG	1320
CAAGTTATTT	TAGACTCGTT	AGCTCAGTTG	GTAGAGCAAT	TGACTTTTAA	TCAATGGGTC	1380
ACTGGTTTCGA	GCCCAGTACG	GGTCATATAT	GCGGGTTTGG	CGGAATTCTA	ATCTCTTTGA	1440
AATCATCTTC	TCTCACTTTC	CAAAACTCTA	TTACCTCTTA	TTATAACCACA	TTTCAATCTT	1500
CAACTTCCCA	GTAATATAAG	CACCTCTGGC	GAAAGAAGTT	TCAATGTCCCT	AAAGTAATAA	1560
GTGAATCCAA	TTCAGGAACCT	CCAAGAACAA	AAGAAACATC	TGGTGTCAAC	AGTATTGGAT	1620
GGCACAGAGT	CACGTGGTAG	TCTGACCCTA	GCAGAAATTT	TAAATAGTAA	ACTATTTACT	1680
GGTTAATTAA	ATGGTTAAAT	AACCGGTTTA	GAAAACTATT	TAATAAAGTA	AAAGAAGTTG	1740
AGAAAAAACT	TCATCATTTA	TTGAAATGAG	GGATTTATGA	AATTTAGTAA	AAAATATATA	1800
GCAGCTGGAT	CAGCTGTTAT	CGTATCCTTG	AGTCTATGTG	CCTATGCACT	AAACCAGCAT	1860
CGTTCGCAGG	AAAATAAGGA	CAATAATCGT	GTCTCTTATG	TGGATGGCAG	CCAGTCAAGT	1920
CAGAAAAGTG	AAAACCTTGAC	ACCAGACCAG	GTTAGCCAGA	AAGAAGGAAT	TCAGGCTGAG	1980
CAAAATTGTAA	TCAAAATTAC	AGATCAGGGC	TATGTAACGT	CACACGGTGA	CCACTATCAT	2040

TACTATAATG	GGAAAGTTCC	TTATGATGCC	CTCTTTAGTG	AAGAACTCTT	GATGAAGGAT	2100
CCAAACTATC	AACTTAAAGA	CGCTGATATT	GTCAATGAAG	TCAAGGGTGG	TTATATCATC	2160
AAGGTCGATG	GAAATATTA	TGTCTACCTG	AAAGATGCAG	CTCATGCTGA	TAATGTTTGA	2220
ACTAAAGATG	AAATCAATCG	TCAAAAACAA	GAACATGTCA	AAGATAATGA	GAAGGTTAAC	2280
TCTAATGTTG	CTGTAGCAAG	GTCTCAGGGA	CGATATACGA	CAAATGATGG	TTATGTCTTT	2340
AATCCAGCTG	ATATTATCGA	AGATACGGGT	AATGCTTATA	TCGTTCTCTA	TGGAGGTCAC	2400
TATCACTACA	TTCCCCAAAG	CGATTTATCT	GCTAGTGAAT	TAGCAGCAGC	TAAAGCACAT	2460
CTGGCTGGAA	AAAATATGCA	ACCGAGTCAG	TTAAGCTATT	CTTCAACAGC	TAGTGACAAT	2520
AACACGCAAT	CTGTAGCAAA	AGGATCAACT	AGCAAGCCAG	CAAATAAATC	TGAAAATCTC	2580
CAGAGTCTTT	TGAAGGAACT	CTATGATTCA	CCTAGCGCCC	AACGTTACAG	TGAATCAGAT	2640
GGCCTGGTCT	TTGACCCTGC	TAAGATTATC	AGTCGTACAC	CAAATGGAGT	TGCGATTCCG	2700
CATGGCGACC	ATTACCACTT	TATTCCTTAC	AGCAAGCTTT	CTGCTTTAGA	AGAAAAGATT	2760
GCCAGAATGG	TGCCATATCAG	TGGAACGGT	TCTACAGTTT	CTACAAATGC	AAAACCTAAT	2820
GAAGTAGTGT	CTAGTCTAGG	CAGTCTTTCA	AGCAATCCTT	CTTCTTTAAC	GACAAGTAAG	2880
GAGCTCTCTT	CAGCATCTGA	TGGTTATATT	TTTAATCCAA	AAGATATCGT	TGAAGAAACG	2940
GCTACAGCTT	ATATTGTAAG	ACATGGTGAT	CATTTCCATT	ACATTTCCAA	ATCAAAATCA	3000
ATTGGGCAAC	CGACTCTTCC	AAACAATAGT	CTAGCAACAC	CTTCTCCATC	TCTTCCAATC	3060
AATCCAGGAA	CTTCACATGA	GAAACATGAA	GAAGATGGAT	ACGGATTGTA	TGCTAATCGT	3120
ATTATCGCTG	AAGATGAATC	AGGTTTGTGC	ATGAGTCACG	GAGACCACAA	TCATTATTTC	3180
TTCAAGAAGG	ACTTGACAGA	AGAGCAAATT	AAGGCTGCGC	AAAAACATTT	AGAGGAAGTT	3240
AAAAGTAGTC	ATAATGGATT	AGATTCTTTG	TCATCTCATG	AACAGGATTA	TCCAGGTAAT	3300
GCCAAAGAAA	TGAAAGATTT	AGATAAAAAA	ATCGAAGAAA	AAATTGCTGG	CATTATGAAA	3360
CAATATGGTG	TCAAACGTGA	AAGTATTGTC	GTGAATAAAG	AAAAAATGC	GATTATTTAT	3420
CCGCATGGAG	ATCACCATCA	TGCAGATCCG	ATTGATGAAC	ATAAACCGGT	TGGAATTGGT	3480
CATTCTCACA	GTAACATGA	ACTGTTTAAA	CCCGAAGAA	GAGTTGCTAA	AAAAGAAGGG	3540
AATAAAGTTT	ATACTGGAGA	AGAATTAAAG	AATGTTGTGA	ATTTGTTAAA	AAATAGTACG	3600
TTTAATAATC	AAAACCTTAC	TCTAGCCAAT	GGTCAAAAAC	GCGTTTCTTT	TAGTTTTCCTG	3660
CCTGAATTGG	AGAAAAAATT	AGGTATCAAT	ATGCTAGTAA	AATTAATAAC	ACCAGATGGA	3720
AAAGTATTGG	AGAAAGTATC	TGGTAAAGTA	TTTGGAGAAG	GAGTAGGGAA	TATTGCAAAC	3780
TTTGAATTAG	ATCAACCTTA	TTTACCAGGA	CAAACATTTA	AGTATACTAT	CGCTTCAAAA	3840
GATTATCCAG	AAGTAAGTTA	TGATGGTACA	TTTACAGTTC	CAACCTCTTT	AGCTTACAAA	3900
ATGGCCAGTC	AAACGATTTT	CTATCCTTTC	CATGCAGGGG	ATACTTATTT	AAGAGTGAAC	3960
CCTCAATTTG	CAGTGCCTAA	AGGAACTGAT	GCTTTAGTCA	GAGTGTTTGA	TGAATTTCAT	4020
GGAAATGCTT	ATTTAGAAAA	TAACATAAAA	GTTGGTGAAA	TCAAATTACC	GATTCCGAAA	4080
TTAAACCAAG	GAACAACCAG	AACGGCCGGA	AATAAAATTC	CTGTAACCTT	CATGGCAAAT	4140
GCTTATTTGG	ACAATCAATC	GACTTATATT	GTGGAAAGTAC	CTATCTTGGA	AAAAGAAAAAT	4200
CAAACTGATA	AACCAAGTAT	TCTACCACAA	TTTAAAAGGA	ATAAAGCACA	AGAAAACCTCA	4260
AAACTTGATG	AAAAGGTAGA	AGAACCAAAG	ACTAGTGAGA	AGGTAGAAAA	AGAAAACTTT	4320
TCTGAAACTG	GGAATAGTAC	TAGTAATTCA	ACGTTAGAAG	AAGTTCTTAC	AGTGGATCCT	4380
GTACAAGAAA	AAGTAGCAAA	ATTTGCTGAA	AGTTATGGGA	TGAAGCTAGA	AAATGTCTTG	4440
TTTAATATGG	ACGGAACAAT	TGAATTATAT	TTACCATCAG	GAGAAGTCAT	TAAAAAGAAT	4500
ATGGCAGATT	TTACAGGAGA	AGCACCTCAA	GGAAATGGTG	AAAATAAACC	ATCTGAAAAT	4560
GGAAAAGTAT	CTACTGGAAC	AGTTGAGAAC	CAACCAACAG	AAAATAAACC	AGCAGATTCT	4620
TTACCAGAGG	CACCAAACGA	AAAACCTGTA	AAACCAGAAA	ACTCAACGGA	TAATGGAATG	4680
TTGAATCCAG	AAGGGAATGT	GGGGAGTGAC	CCTATGTTAG	ATCCAGCATT	AGAGGAAGCT	4740

CCAGCAGTAG ATCCTGTACA AGAAAAATTA GAAAAATTTA CAGCTAGTTA CGGATTAGGC	4800
TTAGATAGTG TTATATTCAA TATGGATGGA ACGATTGAAT TAAGATTGCC AAGTGGAGAA	4860
GTGATAAAAA AGAATTTATC TGATTTTATA GCGTAAGGAA TAGCAGTAGA AAAAGTCTGA	4920
ATCAAAAAATG AAGTTCTCTC AAAAGTTAGA AATAAACTC TGACTTTGGG AGAATTTTCAT	4980
TTTATTATTA ATATATAAAA TTTCTTGACA TACAACCTAA AAAGAGGTGG AATATTTACT	5040
AGTTAATT (SEQ ID NO : 2)	5048

FIGURE 2

ATGAAAATCA ATAAAAAATA TCTAGCTGGG TCAGTAGCTA CACTTGTTTT AAGTGTCTGT	60
GCTTATGAAC TAGGTTTGCA TCAAGCTCAA ACTGTAAAAG AAAATAATCG TGTTCCTAT	120
ATAGATGGAA AACAAGCGAC GCAAAAAACG GAGAATTTGA CTCCTGATGA GGTAGCAAG	180
CGTGAAGGAA TCAACGCCGA ACAAAATCGTC ATCAAGATTA CGGATCAAGG TTATGTGACC	240
TCTCATGGAG ACCATTATCA TTAATAAAT GGCAAGGTCC CTTATGATGC CATCATCAGT	300
GAAGAGCTCC TCATGAAAGA TCCGAATTAT CAGTTGAAGG ATTCAGACAT TGTCAATGAA	360
ATCAAGGGTG GTTATGTCAT TAAGGTAAAC GGTAAATACT ATGTTTACCT TAAGGATGCA	420
GCTCATGCCG ATAATGTCCG TACAAAAGAA GAAATCAATC GGCAAAAACA AGAACATAGT	480
CAGCATCGTG AAGGAGGGAC TTCAGCAAAC GATGGTGCGG TAGCCTTTGC ACGTTCACAG	540
GGACGCTACA CCACAGATGA TGGTTATATC TTCAATGCAT CTGATATCAT CGAAGATACG	600
GGCGATGCCT ATATCGTTCC TCATGGAGAT CATTACCATT ACATTCCTAA GAATGAGTTA	660
TCAGCTAGCG AGTTGGCTGC TGCAGAAGCC TTCCTATCTG GTCGGGAAAA TCTGTCAAAT	720
TTAAGAACCCT ATCGCCGACA AAATAGCGAT AACACTCCAA GAACAACTG GGTACCTTCT	780
GTAAGCAATC CAGGAACCTAC AAATACTAAC ACAAGCAACA ACAGCAACAC TAACAGTCAA	840
GCAAGTCAAA GTAATGACAT TGATAGTCTC TTGAAACAGC TCTACAACT GCCTTTGAGT	900
CAACGCCATG TAGAATCTGA TGGCCTTATT TTCGACCCAG CGCAAATCAC AAGTCGAACC	960
GCCAGAGGTG TAGCTGTCCC TCATGGTAAC CATTACCATT TTATCCCTTA TGAACAAATG	1020
TCTGAATTGG AAAAACGAAT TGCTCGTATT ATTCCCCTTC GTTATCGTTC AAACCATTGG	1080
GTACCAGATT CAAGACCAGA AGAACCAAGT CCACAACCGA CTCCAGAACC TAGTCCAAGT	1140
CCGCAACCTG CACCAAATCC TCAACCAGCT CCAAGCAATC CAATTGATGA GAAATTGGTC	1200
AAAGAAGCTG TTCGAAAAGT AGGCGATGGT TATGTCTTTG AGGAGAATGG AGTTTCTCGT	1260
TATATCCCAG CCAAGAATCT TTCAGCAGAA ACAGCAGCAG GCATTGATAG CAACTGGCC	1320
AAGCAGGAAA GTTTATCTCA TAAGCTAGGA GCTAAGAAAA CTGACCTCCC ATCTAGTGAT	1380
CGAGAATTTT ACAATAAGGC TTATGACTTA CTAGCAAGAA TTCACCAAGA TTTACTTGAT	1440
AATAAAGGTC GACAAGTTGA TTTTGAGGCT TTGGATAACC TGTGGAACG ACTCAAGGAT	1500
GTCTCAAGTG ATAAAGTCAA GTTAGTGGAT GATATTCCTG CCTTCTTAGC TCCGATTCGT	1560
CATCCAGAAC GTTTAGGAAA ACCAAATGCG CAAATTACCT AACTGATGA TGAGATTCAA	1620
GTAGCCAAGT TGGCAGGCAA GTACACAACA GAAGACGGTT ATATCTTTGA TCCTCGTGAT	1680
ATAACCAGTG ATGAGGGGGA TGCCATATGTA ACTCCACATA TGACCCATAG CCACTGGATT	1740
AAAAAAGATA GTTTGTCTGA AGCTGAGAGA GCGGCAGCCC AGGCTTATGC TAAAGAGAAA	1800
GGTTTGACCC CTCCTTCGAC AGACCATCAG GATTGAGGAA ATACTGAGGC AAAAGGAGCA	1860
GAAGCTATCT ACAACCGCGT GAAAGCAGCT AAGAAGGTGC CACTTGATCG TATGCCTTAC	1920
AATCTTCAAT ATACTGTAGA AGTCAAAAAC GGTAGTTTAA TCATACCTCA TTATGACCAT	1980
TACCATAACA TCAAATTTGA GTGGTTTGAC GAAGGCCCTT ATGAGGCACC TAAGGGGTAT	2040
ACTCTGAGG ATCTTTTGGC GACTGTCAAAG TACTATGTCG AACATCCAAA CGAACGTCCG	2100
CATTCAGATA ATGGTTTGG TAACGCTAGC GACCATGTTC AAAGAAACAA AAATGGTCAA	2160

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GCTGATACCA ATCAAACGGA AAAACCAAGC GAGGAGAAAC CTCAGACAGA AAAACCTGAG	2220
GAAGAAACCC CTCGAGAAGA GAAACCACAA AGCGAGAAAC CAGAGTCTCC AAAACCAACA	2280
GAGGAACCAG AAGAAGAATC ACCAGAGGAA TCAGAAGAAC CTCAGGTCGA GACTGAAAAG	2340
GTTGAAGAAA AACTGAGAGA GGCTGAAGAT TTACTTGGAA AAATCCAGGA TCCAATTATC	2400
AAGTCCAATG CCAAAGAGAC TCTCACAGGA TTAAAAATA ATTTACTATT TGGCACCCAG	2460
GACAACAATA CTATTATGGC AGAAGCTGAA AAATATTGG CTTTATTTAA GGAGAGTAAG	2520
TAA (SEQ ID NO: 3)	2523

FIGURE 3

CAGAGATCTT AGTGAATCAA ATATACTTAA GAAAAGAGGA AAGAATGAAA ATCAATAAAA	60
AATATCTAGC TGGGTCAGTA GCTACACTTG TTTTAAGTGT CTGTGCTTAT GAACTAGGTT	120
TGCATCAAGC TCAAACGTGA AAAGAAAATA ATCGTGTTC CTATATAGAT GGAAAACAAG	180
CGACGCAAAA AACGGAGAAT TTGACTCCTG ATGAGGTTAG CAAGCGTGAA GGAATCAACC	240
CCGAACAAAT CGTCATCAAG ATTACGGATC AAGGTTATGT GACCTCTCAT GGAGACCATT	300
ATCATTACTA TAATGGCAAG GTCCCTTATG ATGCCATCAT CAGTGAAGAG CTCCTCATGA	360
AAGATCCGAA TTATCAGTTG AAGGATTCAG ACATTGTCAA TGAAATCAAG GGTGGTTATG	420
TCATTAAGGT AAACGGTAAA TACTATGTTT ACCTTAAGGA TGCAGCTCAT GCGGATAATG	480
TCCGTACAAA AGAAGAAATC AATCGGCAAA AACAAGAACA TAGTCAGCAT CGTGAAGGAG	540
GGACTTCAGC AAACGATGGT GCGGTAGCCT TTGCACGTTT ACAGGGACGC TACACCACAG	600
ATGATGGTTA TATCTTCAAT GCATCTGATA TCATCGAAGA TACGGGCGAT GCCTATATCG	660
TTCTTCATGG AGATCATTAC CATTACATTC CTAAGAATGA GTTATCAGCT AGCGAGTTGG	720
CTGCTGCAGA AGCCTTCCTA TCTGGTCGGG AAAATCTGTC AAATTTAAGA ACCTATCGCC	780
GACAAAATAG CGATAACACT CCAAGAACAA ACTGGGTACC TTCTGTAAGC AATCCAGGAA	840
CTACAAATAC TAACACAAGC AACAACAGCA AACTAACAG TCAAGCAAGT CAAAGTAATG	900
ACATTGATAG TCTCTTGAAA CAGCTCTACA AACTGCCTTT GAGTCAACGC CATGTAGAAT	960
CTGATGGCCT TATTTTCGAC CCAGCGCAAA TCACAAGTCG AACC GCCAGA GGTGTAGCTG	1020
TCCCTCATGG TAACCATTAC CACTTTATCC CTTATGAACA AATGTCTGAA TTGGAAAAC	1080
GAATTGCTCG TATTATTCCC CTTCGTTATC GTTCAAACCA TTGGGTACCA GATTCAAGAC	1140
CAGAAGAACC AAGTCCACAA CCGACTCCAG AACCTAGTCC AAGTCCGCAA CCTGCACCAA	1200
ATCCTCAACC AGCTCCAAGC AATCCAATTG ATGAGAAATT GGTCAAAGAA GCTGTTTCGAA	1260
AAGTAGGCGA TGGTTATGTC TTTGAGGAGA ATGGAGTTTC TCGTTATATC CCAGCCAAGA	1320
ATCTTTCAGC AGAAACAGCA GCAGGCATTG ATAGCAAACCT GGCCAAGCAG GAAAGTTTAT	1380
CTCATAAGCT AGGAGCTAAG AAAACTGACC TCCCATCTAG TGATCGAGAA TTTTACAATA	1440
AGGCTTATGA CTTACTAGCA AGAATTCACC AAGATTTACT TGATAATAAA GGTCGACAAG	1500
TTGATTTTGA GGCTTTGGAT AACCTGTTGG AACGACTCAA GGATGTCTCA AGTGATAAAG	1560
TCAAGTTAGT GGATGATATT CTTGCCTTCT TAGCTCCGAT TCGTCATCCA GAACGTTTAG	1620
GAAAACCAAA TGCGCAAATT ACCTACACTG ATGATGAGAT TCAAGTAGCC AAGTTGGCAG	1680
GCAAGTACAC AACAGAAGAC GGTATATCTT TTGATCCTCG TGATATAACC AGTGATGAGG	1740
GGGATGCCTA TGTAACCTCA CATATGACCC ATAGCCACTG GATTAAAAAA GATAGTTTGT	1800
CTGAAGCTGA GAGAGCGGCA GCCCAGGCTT ATGCTAAAGA GAAAGGTTTG ACCCTCCTT	1860
CGACAGACCA TCAGGATTCA GGAAATACTG AGGCAAAAGG AGCAGAAGCT ATCTACAACC	1920
GCGTGAAAGC AGCTAAGAAG GTGCCACTTG ATCGTATGCC TTACAATCTT CAATATACTG	1980
TAGAAGTCAA AAACGGTAGT TTAATCATAC CTCATTATGA CCATTACCAT AACATCAAAT	2040
TTGAGTGGTT TGACGAAGGC CTTTATGAGG CACCTAAGGG GTATACTCTT GAGGATCTTT	2100

TGGCGACTGT	CAAGTACTAT	GTCGAACATC	CAAACGAACG	TCCGCATTCA	GATAATGGTT	2160
TTGGTAACGC	TAGCGACCAT	GTTCAAAGAA	ACAAAAATGG	TCAAGCTGAT	ACCAATCAAA	2220
CGGAAAAACC	AAGCGAGGAG	AAACCTCAGA	CAGAAAAACC	TGAGGAAGAA	ACCCCTCGAG	2280
AAGAGAAACC	ACAAAGCGAG	AAACCAGAGT	CTCCAAAACC	AACAGAGGAA	CCAGAAGAAG	2340
AATCACCAGA	GGAATCAGAA	GAACCTCAGG	TCGAGACTGA	AAAGGTTGAA	GAAAAACTGA	2400
GAGAGGCTGA	AGATTTACTT	GGAAAAATCC	AGGATCCAAT	TATCAAGTCC	AATGCCAAAG	2460
AGACTCTCAC	AGGATTAAAA	AATAATTTAC	TATTTGGCAC	CCAGGACAAC	AATACTATTA	2520
TGGCAGAAGC	TGAAAACTA	TTGGCTTTAT	TAAAGGAGAG	TAAGTAAAGG	TAGCAGCATT	2580
TTCTAACTCC	TAAAAACAGG	ATAGGAGAAC	GGGAAAACGA	AAAATGAGAG	CAGAATGTGA	2640
GTTCTAG	(SED ID NO : 4)					2647

FIGURE 4

GGGTCTTAAA	ACTCTGAATC	CTTTAGAGGC	AGACCCACAA	AATGACAAGA	CCTATTTAGA	60
AAATCTGGAA	GAAAATATGA	GTGTTCTAGC	AGAAGAATTA	AAGTGAGGAA	AGAATGAAAA	120
TCAATAAAAA	ATATCTAGCA	GGTTCAGTGG	CAGTCCCTGC	CCTAAGTGTT	TGTTCCCTATG	180
AACTTGGTCG	TCACCAAGCT	GGTCAGGTTA	AGAAAGAGTC	TAATCGAGTT	TCTTATATAG	240
ATGTTGATCA	GGCTGGTCAA	AAGGCAGAAA	ATTTGACACC	AGATGAAGTC	AGTAAGAGAG	300
AGGGGATCAA	CGCCGAACAA	ATTGTTATCA	AGATTACGGA	TCAAGGTTAT	GTGACCTCTC	360
ATGGAGACCA	TTATCATTAC	TATAATGGCA	AGGTTCCCTTA	TGATGCCATC	ATCAGTGAAG	420
AACTTCTCAT	GAAAGATCCG	AATTATCAGT	TGAAGGATTC	AGACATTGTC	AATGAAATCA	480
AGGGTGGCTA	TGTGATTAAG	GTAGACGGAA	AATACTATGT	TTACCTTAAA	GATGCGGCCC	540
ATGCGGACAA	TATTCGGACA	AAAGAAGAGA	TTAAACGTCA	GAAGCAGGAA	CACAGTCATA	600
ATCATAACTC	AAGAGCAGAT	AATGCTGTTG	CTGCAGCCAG	AGCCCAAGGA	CGTTATACAA	660
CGGATGATGG	GTATATCTTC	AATGCATCTG	ATATCATTGA	GGACACGGGT	GATGCTTATA	720
TCGTTCTCTA	CGGCGACCAT	TACCATTACA	TTCCTAAGAA	TGAGTTATCA	GCTAGCGAGT	780
TAGCTGCTGC	AGAAGCCTAT	TGGAATGGGA	AGCAGGGATC	TCGTCCTTCT	TCAAGTTCTA	840
GTTATAATGC	AAATCCAGTT	CAACCAAGAT	TGTCAGAGAA	CCACAATCTG	ACTGTCACTC	900
CAACTTATCA	TCAAAATCAA	GGGGAAAAACA	TTTCAAGCCT	TTTACGTGAA	TTGTATGCTA	960
AACCCTTATC	AGAACGCCAT	GTAGAATCTG	ATGGCCTTAT	TTTCGACCCA	GCGCAAATCA	1020
CAAGTCGAAC	CGCCAGAGGT	GTAGCTGTCC	CTCATGGTAA	CCATTACCAC	TTTATCCCTT	1080
ATGAACAAAT	GTCTGAATTG	GAAAAACGAA	TTGCTCGTAT	TATTCCTCTT	CGTTATCGTT	1140
CAAACCATTG	GGTACCAGAT	TCAAGACCAG	AACAACCAAG	TCCACAATCG	ACTCCGGAAC	1200
CTAGTCCAAG	TCTGCAACCT	GCACCAAATC	CTCAACCAGC	TCCAAGCAAT	CCAAITGATG	1260
AGAAATTGGT	CAAGAAGCT	GTTCGAAAAG	TAGGCGATGG	TTATGTCTTT	GAGGAGAATG	1320
GAGTTTCTCG	TTATATCCCA	GCCAAGGATC	TTTCAGCAGA	AACAGCAGCA	GGCATTGATA	1380
GCAAACTGGC	CAAGCAGGAA	AGTTTATCTC	ATAAGCTAGG	AGCTAAGAAA	ACTGACCTCC	1440
CATCTAGTGA	TCGAGAATTT	TACAATAAGG	CTTATGACTT	ACTAGCAAGA	ATTACCAAG	1500
ATTTACTTGA	TAATAAAGGT	CGACAAGTTG	ATTTTGAGGT	TTTGGATAAC	CTGTTGGAAC	1560
GACTCAAGGA	TGCTCAAGT	GATAAAGTCA	AGTTAGTGGA	TGATATTCTT	GCCTTCTTAG	1620
CTCCGATTCTG	TCATCCAGAA	CGTTTAGGAA	AACCAAATGC	GCAAATTACC	TACACTGATG	1680
ATGAGATTCA	AGTAGCCAAG	TTGGCAGGCA	AGTACACAAC	AGAAGACGGT	TATATCTTTG	1740
ATCCTCGTGA	TATAACCAGT	GATGAGGGGG	ATGCCTATGT	AACTCCACAT	ATGACCCATA	1800
GCCACTGGAT	TAAAAAAGAT	AGTTTGTCTG	AAGCTGAGAG	AGCGGCAGCC	CAGGCTTATG	1860
CTAAAGAGAA	AGGTTTGACC	CCTCCTTCGA	CAGACCACCA	GGATTCAGGA	AATACTGAGG	1920

CAAAAGGAGC	AGAAGCTATC	TACAACCGCG	TGAAAGCAGC	TAAGAAGGTG	CCACTTGATC	1980
GTATGCCTTA	CAATCTTCAA	TATACTGTAG	AAGTCAAAAA	CGGTAGTTTA	ATCATACCTC	2040
ATTATGACCA	TTACCATAAC	ATCAAATTTG	AGTGGTTTGA	CGAAGGCCTT	TATGAGGCAC	2100
CTAAGGGGTA	TAGTCTTGAG	GATCTTTTGG	CGACTGTCAA	GTACTATGTC	GAACATCCAA	2160
ACGAACGTCC	GCATTCAGAT	AATGGTTTTG	GTAACGCTAG	TGACCATGTT	CGTAAAAATA	2220
AGGCAGACCA	AGATAGTAAA	CCTGATGAAG	ATAAGGAACA	TGATGAAGTA	AGTGAGCCAA	2280
CTCACCTGA	ATCTGATGAA	AAAGAGAATC	ACGCTGGTTT	AAATCCTTCA	GCAGATAATC	2340
TTTATAAACC	AAGCACTGAT	ACGGAAGAGA	CAGAGGAAGA	AGCTGAAGAT	ACCACAGATG	2400
AGGCTGAAAT	TCCTCAAGTA	GAGAATTCTG	TTATTAACGC	TAAGATAGCA	GATGCGGAGG	2460
CCTTGCTAGA	AAAAGTAACA	GATCCTAGTA	TTAGACAAAA	TGCTATGGAG	ACATTGACTG	2520
GTCTAAAAAG	TAGTCTTCTT	CTCGGAACGA	AAGATAATAA	CACTATTTCA	GCAGAAGTAG	2580
ATAGTCTCTT	GGCTTTGTTA	AAAGAAAGTC	AACCGGCTCC	TATACAGTAG	TAAAATGAA	2639

(SEQ ID NO : 5)

FIGURE 5

MKFSKKYIAA	GSAVIVSLSL	CAYALNQHRS	QENKDNRRVS	YVDGSQSSQK	50
SENLTDPQVS	QKEGIQAEQI	VIKITDQGYV	TSHGDHYHYV	NGKVPYDALF	100
SEELLMKDPN	YQLKDADIVN	EVKGGYIIKV	DGKYVYVLKD	AAHADNVRTK	150
DEINRQKQEH	VKDNEKVNSN	VAVARSQGRY	TTNDGYVFNP	ADIIEDTGNA	200
YIVPHGGHYH	YIPKSDLSAS	ELAAAKAHLA	GKNMQPSQLS	YSSTASDNNT	250
QSVAKGSTSK	PANKSENLOS	LLKELYDSPS	AQRYSESDGL	VFDPAKIISR	300
TPNGVAIPHG	DHYHFIPYSK	LSALEEKIAR	MVPISGTGST	VSTNAKPNEV	350
VSSLGSLSSN	PSSLTTSKEL	SSASDGYIFN	PKDIVEETAT	AYIVRHGDHF	400
HYIPKSNQIG	QPTLPNNSLA	TPSPSLPINP	GTSHEKHEED	GYGFDANRII	450
AEDESGFVMS	HGDHNHYFFK	KDLTEEQIKA	AQKHLEEVKT	SHNGLDSLSS	500
HEQDYPGNAK	EMKDLDDKIE	EKIAGIMKQY	GVKRESIVVN	KEKNALIYPH	550
GDHHHADPID	EHKPVGIGHS	HSNYELFKPE	EGVAKKEGK	VYTGEELTNV	600
VNLLKNSTFN	NQNFTLANGQ	KRVSFSPPE	LEKKLGINML	VKLITPDGKV	650
LEKVSQKVFQ	EGVGNIANFE	LDQPYLPGQT	FKYTIASKDY	PEVSYDGTFT	700
VPTSLAYKMA	SQTIFYPFHA	GDTYLRVNPQ	FAVPKGTDAL	VRVFDEFHGN	750
AYLENNYKVG	EIKLPIPKLN	QGTTRTAGNK	IPVTFMANAY	LDNQSTYIVE	800
VPILEKENQT	DKPSILPQFK	RNKAQENSKL	DEKVEEPKTS	EKVEKEKLSE	850
TGNSTSNSTL	EEVPTVDPVQ	EKVAKFAESY	GMKLENVLFN	MDGTIELYLP	900
SGEVIKKNMA	DFTGEAPQGN	GENKPSENGK	VSTGTVENQP	TENKPADSLP	950
EAPNEKPVKP	ENSTDNGMLN	PEGNVGSDPM	LDPALEEAPA	VDPVQEKLEK	1000
FTASYGLGLD	SVIFNMDGTI	ELRLPSGEVI	KKNLSDFIA	(SEQ ID NO: 6)	1039

FIGURE 6

MKINKKYLGA	SVATLVLSVC	AYELGLHQAQ	TVKENNRVS	IDGKQATQKT	50
ENLTPDEVSK	REGINAEQIV	IKITDQGYVT	SHGDHYHYVN	GKVPYDAIIS	100
EELLMKDPNY	QLKDSDIVNE	IKGGYVIKVN	GKYYVYLKDA	AHADNVRTKE	150
EINRQKQEH	QHREGGTSAN	DGAVAFARSQ	GRYTTDDGYI	FNASDIIEDT	200
GDAYIVPHGD	HYHYIPKNEL	SASELAAAEA	FLSGRENLSN	LRTYRRQNSD	250

NTPRTNWWPS	VSNPGTTNTN	TSNNSNTNSQ	ASQSNDDISL	LKQLYKLPLS	300
QRHVESDGLI	FDPAQITSRT	ARGVAVPHGN	HYHFIPYEQM	SELEKRIARI	350
IPLRYRSNHW	VPDSRPEEPS	PQPTPEPSPS	PQPAPNPQPA	PSNFIDEKLV	400
KEAVRKVGDG	YVFEENGVS	YIPAKNLSAE	TAAGIDSKLA	KQESLSHKL	450
AKKTDLPSSD	REFYNKAYDL	LARIHQDILL	NKGRQVDFEA	LDNLLERLKD	500
VSSDKVKLVD	DILAFLAPIR	HPERLGKPN	QITYTDDEIQ	VAKLAGKYTT	550
EDGYIFDPRD	ITSDEGDAYV	TPHMTSHWI	KKDSLSEAER	AAAQAYAKEK	600
GLTPPSTDHQ	DSGNTEAKGA	EAIYNRVKAA	KKVPLDRMPY	NLQYTVEVKN	650
GSLIIPHYDH	YHNIKFEWFD	EGLYEAPKGY	TLEDLLATVK	YYVEHPNERP	700
HSDNGFGNAS	DHVQRNKNQ	ADTNQTEKPS	EEKPQTEKPE	EETPREEKPQ	750
SEKPESPKPT	EEPEEESPEE	SEEPQVETEK	VEEKLREAED	LLGKIQDPPI	800
KSNAKETLTG	LKNNLLFGTQ	DNNTIMAEAE	KLLALLKESK	(SEQ ID NO: 7)	840

FIGURE 7

MKINKKYL	SVAVLALSVC	SYELGRHQAG	QVKKESNRVS	YIDGDQAGQK	50
AENLTPDEV	KREGINAEQI	VIKITDQGYV	TSHGDHYHY	NGKVPYDAII	100
SEELLMKDP	YQLKDSDIVN	EIKGGYVIKV	DGKYVYVLKD	AAHADNIRTK	150
EEIKRQKQEH	SHNHNSRADN	AVAAAAAQGR	YTDDGYIFN	ASDIIEDTGD	200
AYIVPHGDHY	HYIPKNELSA	SELAAAEAYW	NGKQGSRPSS	SSSYNANPVQ	250
PRLSENHNLT	VTPTYHQNQ	ENISSLLREL	YAKPLSERHV	ESDGLIFDPA	300
QITSRTARGV	AVPHGNHYHF	IPYEQMSELE	KRIARIIPLR	YRSNHWVPDS	350
RPEQPSPQST	PEPSPSLQPA	PNPQPAPSNP	IDKLVKEAV	RKVGDCYVFE	400
ENGVSRYIPA	KDLSAETAAG	IDSKLAKQES	LSHKLGA	KKT DLPSSDREFY	450
NKAYDLLARI	HQDLLDNKGR	QVDFEVL	LDNL LERLKD	VSSD KVKLVDDILA	500
FLAPIRHPER	LGKPN	AQITY TDDEIQ	VAKL AGKYT	TEDGY IFDPRD	ITSD 550
EGDAYVTPHM	THSHWIKKDS	LSEAERAAAQ	AYAKEKGLTP	PSTDHQDSGN	600
TEAKGAEAIY	NRVKA	AKKVP LDRMPY	NLQY TVEVK	NGSLI IPHYDHYHNI	650
KFEWFDEGLY	EAPKGYSLED	LLATVKY	YVE HPNERPHSDN	GFGNASDHVR	700
KNKADQDSKP	DEDKEHDEVS	EPHPESDEK	ENHAGLNPSA	DNLYKPSTDT	750
EETEEEEAEDT	TDEAEIPQVE	NSVINAKIAD	AEALLEK	VTD PSIRQ	NAMET 800
LTGLKSSLLL	GTKDNNTISA	EVDSLLALLK	ESQPAPIQ		838

(SEQ ID NO : 8)

FIGURE 8

TGTGCCTATG	CACTAAACCA	GCATCGTTCG	CAGGAAAATA	AGGACAATAA	TCGTGTCTCT	60
TATGTGGATG	GCAGCCAGTC	AAGTCAGAAA	AGTGAAACT	TGACACCAGA	CCAGGTTAGC	120
CAGAAAGAAG	GAATTCAGGC	TGAGCAAATT	GTAATCAAAA	TTACAGATCA	GGGCTATGTA	180
ACGTCACACG	GTGATCACTA	TCATTACTAT	AATGGGAAAG	TTCCTTATGA	TGCCCTCTTT	240
AGTGAAGAAC	TCTTGATGAA	GGATCCAAAC	TATCAACTTA	AAGACGCTGA	TATTGTCAAT	300
GAAGTCAAGG	GTGGTTATAT	CATCAAGGTC	GATGGAAAAT	ATTATGTCTA	CCTGAAAGAT	360
GCAGCTCATG	CTGATAATGT	TCGAACTAAA	GATGAAATCA	ATCGTCAAAA	ACAAGAACAT	420
GTCAAAGATA	ATGAGAAGGT	TAACCTAAT	GTTGCTGTAG	CAAGGTCTCA	GGGACGATAT	480
ACGACAAATG	ATGGTTATGT	CTTAATCCA	GCTGATATTA	TCGAAGATAC	GGGTAATGCT	540

TATATCGTTC	CTCATGGAGG	TCACTATCAC	TACATTCCCA	AAAGCGATTT	ATCTGCTAGT	600
GAATTAGCAG	CAGCTAAAGC	ACATCTGGCT	GGAAAAATA	TGCAACCGAG	TCAGTTAAGC	660
TATTCTTCAA	CACCTTCTCC	ATCTCTTCCA	ATCAATCCAG	GAAC TTCACA	TGAGAAACAT	720
GAAGAAGATG	GATACGGATT	TGATGCTAAT	CGTATTATCG	CTGAAGATGA	ATCAGGTTTT	780
GTCATGAGTC	ACGGAGACCA	CAATCATTAT	TTCTTCAAGA	AGGACTTGAC	AGAAGAGCAA	840
ATTAAGGCTG	CGCAAAAACA	TTTAGAGGAA	GTTAAACTA	GTCATAATGG	ATTAGATTCT	900
TTGTCATCTC	ATGAACAGGA	TTATCCAAGT	AATGCCAAAG	AAATGAAAAG	TTTAGATAAA	960
AAAATCGAAG	AAAAAATTGC	TGGCATTATG	AAACAATATG	GTGTCAAACG	TGAAAGTATT	1020
GTCGTGAATA	AAGAAAAAAA	TGCGATTATT	TATCCGCATG	GAGATCACCA	TCATGCAGAT	1080
CCGATTGATG	AACATAAACC	GGTTGGAATT	GGTCATTCTC	ACAGTAACTA	TGAACTGTTT	1140
AAACCCGAAG	AAGGAGTTGC	TAAAAAAGAA	GGGAATAAAG	TTTATACTGG	AGAAGAATTA	1200
ACGAATGTTG	TTAATTTGTT	AAAAAATAGT	ACGTTTAATA	ATCAAACTT	TACTCTAGCC	1260
AATGGTCAAA	AACGCGTTTC	TTT TAGTTTT	CCGCCTGAAT	TGGAGAAAAA	ATTAGGTATC	1320
AATATGCTAG	TAAAATTAAT	AACACCAGAT	GGAAAAGTAT	TGGAGAAAAG	ATCTGGTAAA	1380
GTATTTGGAG	AAGGAGTAGG	GAATATTGCA	AAC TTTGAAT	TAGATCAACC	TTATTTACCA	1440
GGACAAACAT	TTAAGTATAC	TATCGCTTCA	AAAGATTATC	CAGAAGTAAG	TTATGATGGT	1500
ACATTTACAG	TTCCAACCTC	TTTAGCTTAC	AAAATGGCCA	GTCAAACGAT	TTTCTATCCT	1560
TTCCATGCAG	GGGATACTTA	TTTAAGAGTG	AACCCTCAAT	TTGCAGTGCC	TAAAGGAACT	1620
GATGCTTTAG	TCAGAGTGTT	TGATGAATTT	CATGGAAATG	CTTATTTAGA	AAATAACTAT	1680
AAAGTTGGTG	AAATCAAATT	ACCGATTCCG	AAATTAAACC	AAGGAACAAC	CAGAACGGCC	1740
GGAAATAAAA	TTCTGTAAAC	CTTCATGGCA	AATGCTTATT	TGGACAATCA	ATCGACTTAT	1800
ATTGTGGAAG	TACCTATCTT	GGAAAAAGAA	AATCAAACCTG	ATAAACCAAG	TATTCTACCA	1860
CAATTTAAAA	GGAATAAAGC	ACAAGAAAAC	TCAAAACTTG	ATGAAAAGGT	AGAAGAACCA	1920
AAGACTAGTG	AGAAGGTAGA	AAAAGAAAAA	CTTCTGAAA	CTGGGAATAG	TACTAGTAAT	1980
TCAACGTTAG	AAGAAGTTCC	TACAGTGGAT	CCTGTACAAG	AAAAAGTAGC	AAAATTTGCT	2040
GAAAGTTATG	GGATGAAGCT	AGAAAATGTC	TTGTTTAATA	TGGACGGAAC	AATTGAATTA	2100
TATTTACCAT	CGGGAGAAGT	CATTAAAAAG	AATATGGCAG	ATTTTACAGG	AGAAGCACCT	2160
CAAGGAAATG	GTGAAAATAA	ACCATCTGAA	AATGGAAAAG	TATCTACTGG	AACAGTTGAG	2220
AACCAACCAA	CAGAAAATAA	ACCAGCAGAT	TCTTTACCAG	AGGCACCAAA	CGAAAAACCT	2280
GTAAAACCAG	AAA ACTCAAC	GGATAATGGA	ATGTTGAATC	CAGAAGGGAA	TGTGGGGAGT	2340
GACCC TATGT	TAGATTCAGC	ATTAGAGGAA	GCTCCAGCAG	TAGATCCTGT	ACAAGAAAAA	2400
TTAGAAAAAT	TTACAGCTAG	TTACGGATTA	GGCTTAGATA	GTGTTATATT	CAATATGGAT	2460
GGAACGATTG	AATTAAGATT	GCCAAGTGGA	GAAGTGATAA	AAAAGAATTT	ATTGATCTCA	2520
TAGCGTAA	(SEQ ID NO : 9)					2528

FIGURE 9

CAYALNQHRS	QENKDNRRVS	YVDGSQSSQK	SENLTPDQVS	QKEGIQAEQI	50
VIKITDQGYV	TSHGDHYHYV	NGKVPYDALF	SEELLMKDPN	YQLKDADIVN	100
EVKGGYIIKV	DGKYVYVLKD	AAHADNVRTK	DEINRQKQEH	VKDNEKVNSN	150
VAVARSQGRY	TTNDGYVFNP	ADIIEDTGNA	YIVPHGGHYH	YIPKSDLSAS	200
ELAAAKAHLA	GKNMQPSQLS	YSSTPSPSLP	INPGTSHEKH	EEDGYGFDAN	250
RIIAEDES GF	VMSHGDHNHY	FFKKDLTEEQ	IKAAQKHLEE	VKTSHNGLDS	300
LSSHEQDYP S	NAKEMKDLDK	KIEEKIAGIM	KQYGVKRESI	VVNKEKNAIL	350
YPHGDHHHAD	PIDEHKPVGI	GHSHSNYELF	KPEEGVAKKE	GNKVYTGEEL	400

TNVVNLLKNS TFNNQNFTLA NGQKRVSFSF PPELEKKLGI NMLVKLITPD 450
GKVLEKVS GK VFGEGVG NIA NFELDQPYLP GQTFKYTIAS KDYPEVSYDG 500
TFTVPTSLAY KMASQTIFY FPHAGDTYLRV NPQFAVPKGT DALVRVFDEF 550
HG NAYLENNY KVGEIKLPI KLNQGTTRTA GNKIPVTFMA NAYLDNQSTY 600
IVEVPILEKE NQTDKPSILP QFKRNKAQEN SKLDEKVEEP KTSEKVEKEK 650
LSETGNSTSN STLEEVP TVD PVQEKVAKFA ESYGMKLENV LFNMDGTIEL 700
YLP SGEVIKK NMADFTGEAP QNGENKPS NGKVSTGTVE NQPTENKPAD 750
SLPEAPNEKP VKPENSTDNG MLNPEGNVGS DPMLDSALEE APAVDPVQEK 800
LEKFTASYGL GLDSVIFNMD GTIELRLPSG EVIKKNLLIS 840

(SEQ ID NO : 10)

FIGURE 10

DQGYVTSHGD HYHYNGKVP YDALFSEELL MKDPNYQLKD ADIVNEVKGG YIIKVDGKYY
VYLKDAAHAD NVRTKDEINR QKQEHVKDNE KVNS

(SEQ ID NO: 11)

FIGURE 11

GIQAEQIVIK ITDQGYVTSH GDHYHYNGK VPYDALFSEELL

(SEQ ID NO: 12)

FIGURE 12

TAYIVRHGDH FHYIPKSNQI GQPTLPNNSL ATPSPSLPI

(SEQ ID NO: 13)

FIGURE 13

TSNSTLEEVP TVDPVQEKVA KFAESYGMKL ENVLFN

(SEQ ID NO: 14)

FIGURE 14

MDGTIELRLP SGEVIKKNLS DFIA

(SEQ ID NO: 15)

FIGURE 15

YGLGLDSVIF NMDGTIELRL PSGEVIKKNL SDFIA

(SEQ ID NO: 16)

FIGURE 16

PALEEAPAVD PVQEKLEKFT ASYGLGLDSV IFNMDGTIEL RLPSGEVIKK NLSDFIA

(SEQ ID NO: 17)

FIGURE 17

KVEEPKTSEK VEKEKLSETG NSTSNSTLEE VPTVDPVQEK

(SEQ ID NO: 18)

FIGURE 18

MKDLDKKIEE KIAGIMKQYG VKRESIVVNK EKNAIYYPHG DHHHADPIDE HKPVGIGHSH
SNYELFKPEE GVAKKEGN

(SEQ ID NO: 19)

FIGURE19

AIYYPHGDHH HADPIDEHKP VGIGHSHSNY ELFKPEEGVA KKEGNKVYTG E

(SEQ ID NO: 20)

FIGURE 20

IQVAKLAGKY TTEDGYIFDP RDITSDEGD

(SEQ ID NO: 21)

FIGURE 21

DHQDSGNTA KGAEAIYNRV KAAKKVPLDR MPYNLQYTV VKNGSLIIPH YDHYHNIKFE
WFDEGLYEAP KGYSLEDLLA TVKYYV

(SEQ ID NO: 22)

FIGURE 22

GLYEAPKGYS LEDLLATVKY YVEHPNERPH SDNGFGNASD H

(SEQ ID NO: 23)

FIGURE 23

GLYEAPKGYSLEDLLATVKYYV

(SEQ ID NO: 163)

Figure 24

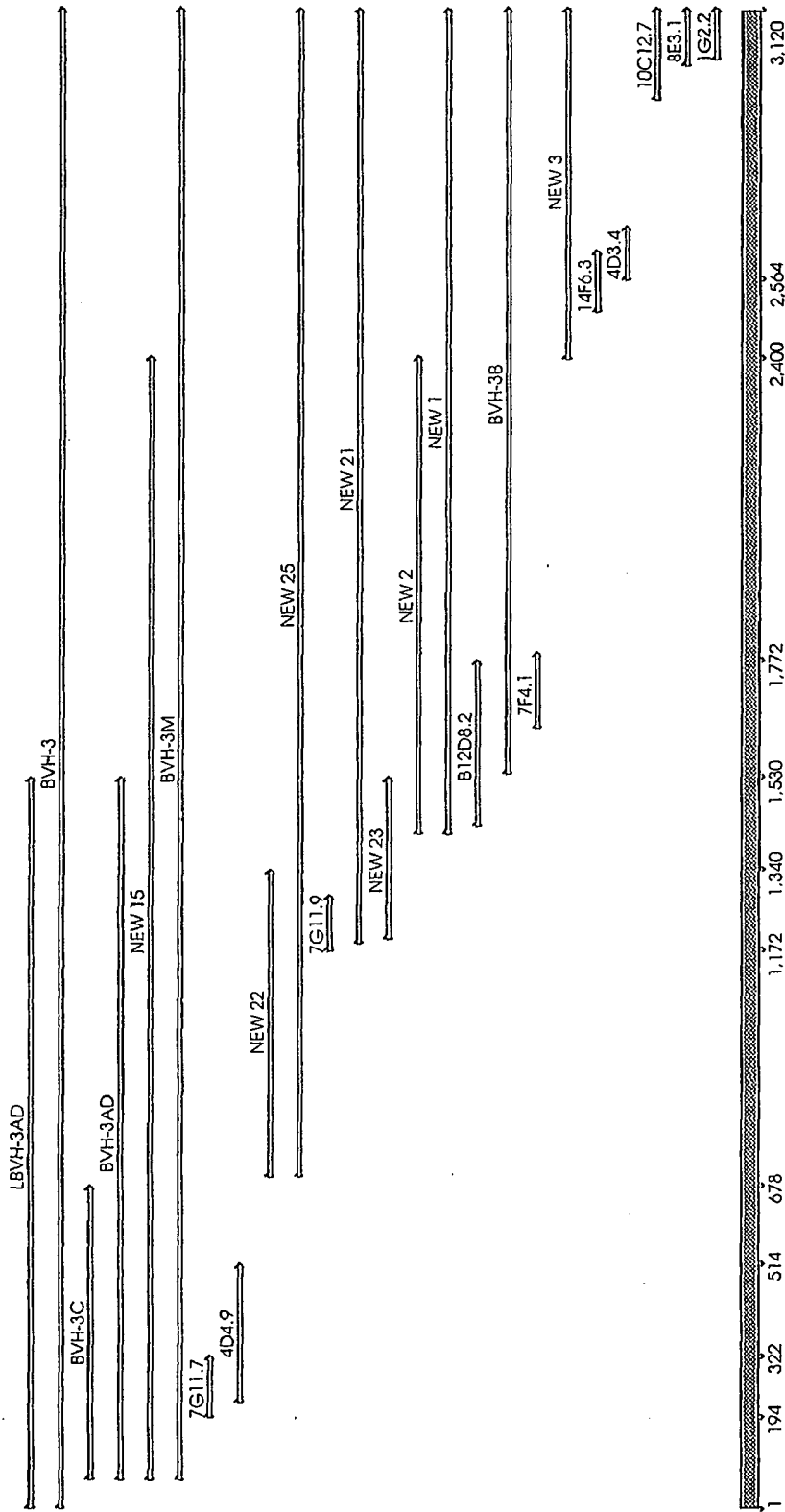


FIGURE 25

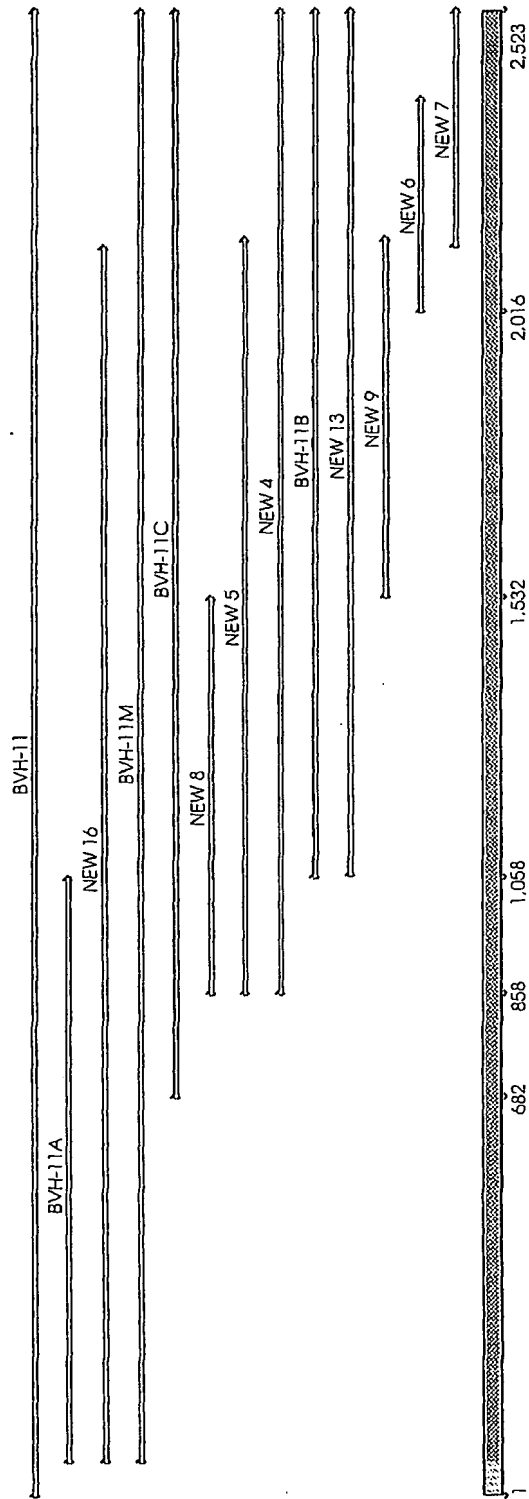


FIGURE 26

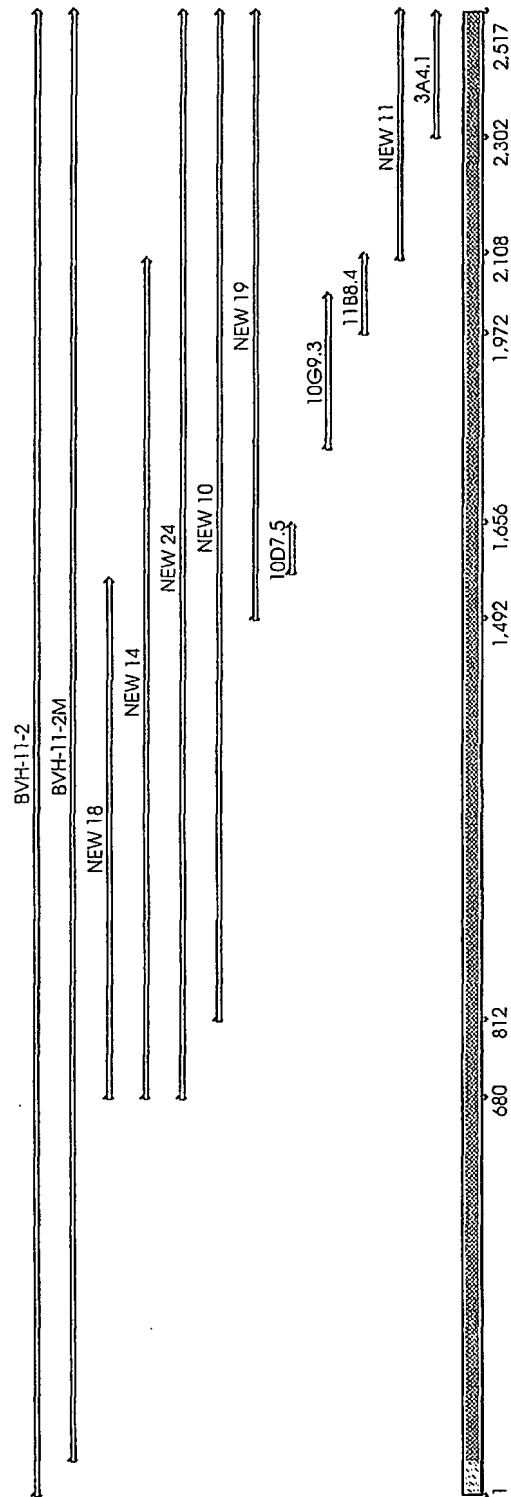


FIGURE 27

Epitope Localization on BVH-3 Protein

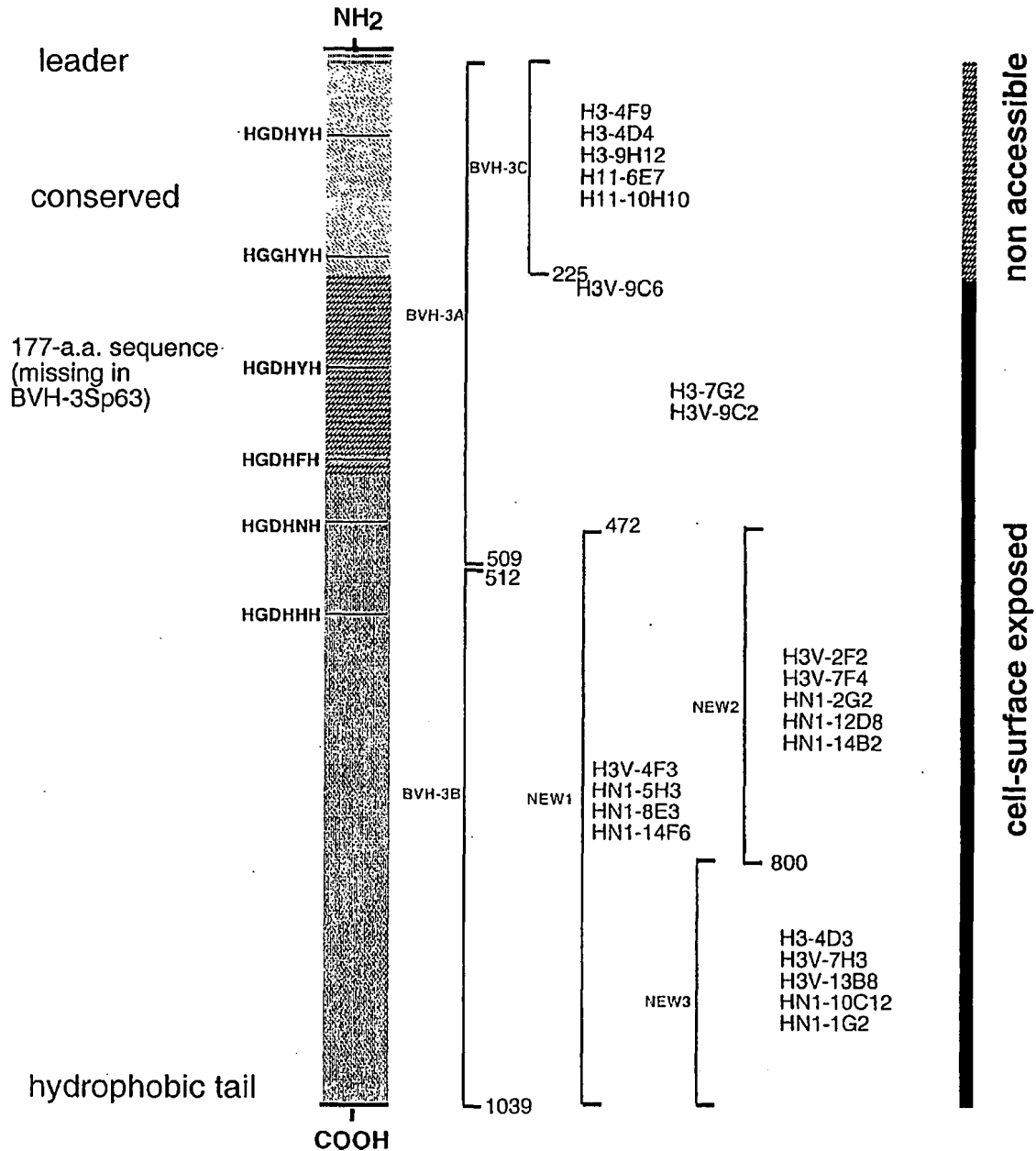
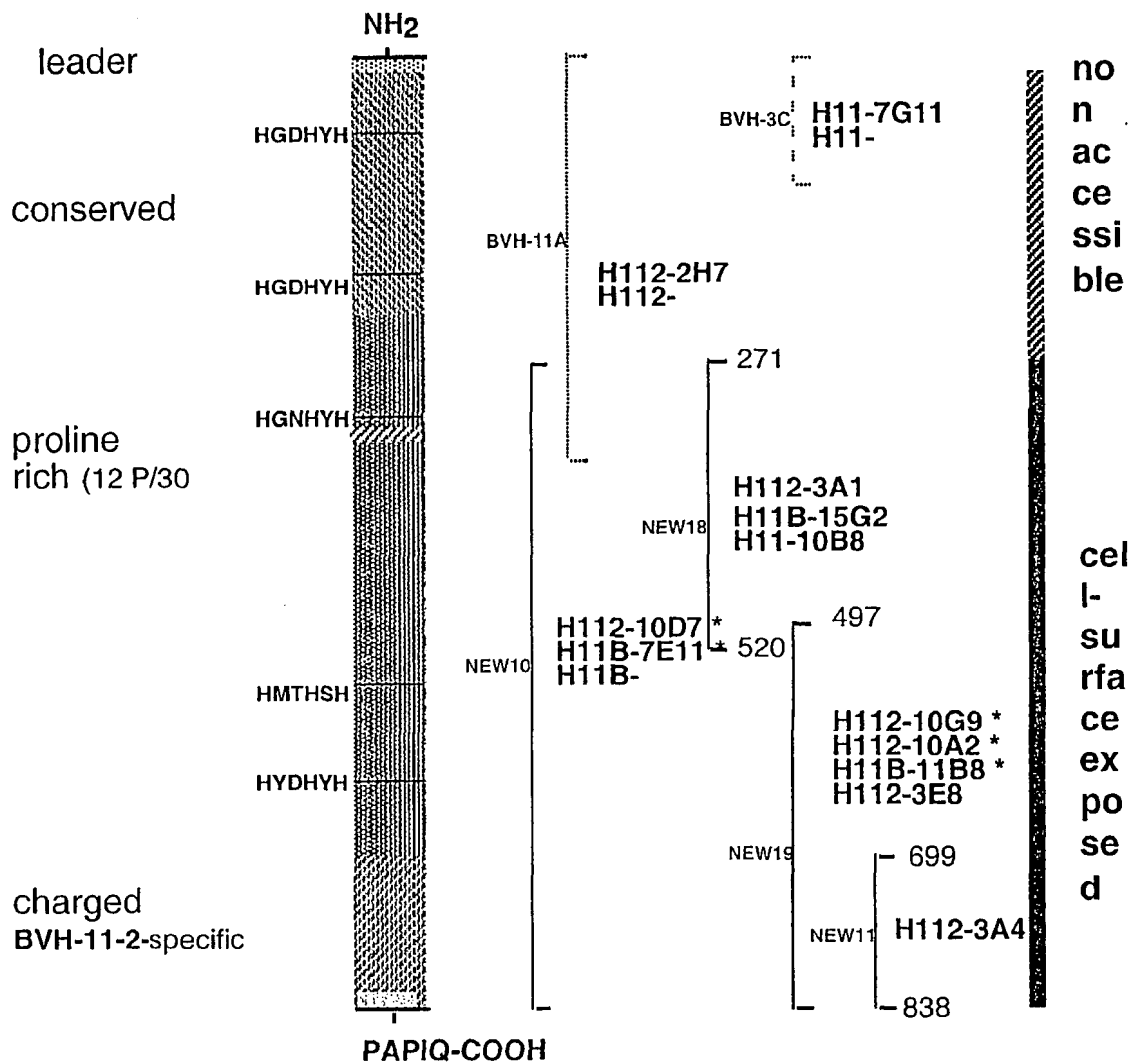


FIGURE 28

Epitope Localization on BVH-11-2 Protein



* Surface-exposed and protection-conferring Mabs

FIGURE 29

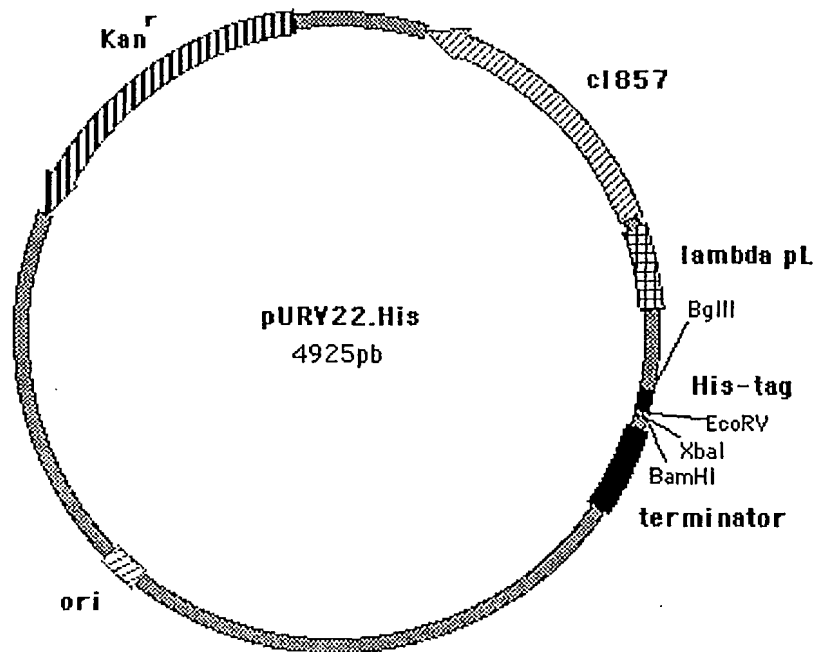


FIGURE 30

BVH-3M	1	CAYALNQHRSQENKDNRRVSYVDGSQSSQKSENLTDPQVSQKEGIQAEQIVIKITDQGYV	60
BVH3-63	1	CAYALNQHRSQENKDNRRVSYVDGSQSSQKSENLTDPQVSQKEGIQAEQIVIKITDQGYV	60

BVH-3M	61	TSHGDHYHYNGKVPYDALFSEELLMKDPNYQLKDADIVNEVKGGYI IKVDGKYYVYLKD	120
BVH3-63	61	TSHGDHYHYNGKVPYDALFSEELLMKDPNYQLKDADIVNEVKGGYI IKVDGKYYVYLKD	120

BVH-3M	121	AAHADNVRTKDEINRQKQEHVKDNEKVNSNVAVARSQGRYT'TNDGYVFNPAIIEDTGNA	180
BVH3-63	121	AAHADNVRTKDEINRQKQEHVKDNEKVNSNVAVARSQGRYT'TNDGYVFNPAIIEDTGNA	180

BVH-3M	181	YIVPHGGHYHYIPKSDLSASELAAAKAHLAGKNMQPSQLSYSSSTASDNNTQSVAKGSTSK	240
BVH3-63	181	YIVPHGGHYHYIPKSDLSASELAAAKAHLAGKNMQPSQLSYSS-----	223

BVH-3M	241	PANKSENLSQLLKELYDSPSAQRYSES DGLVFDPAKII SRTPNGVAIPHGDHYHFIPYSK	300
BVH3-63	224	-----	223
BVH-3M	301	LSALEEKIARMVPISGTGSTVSTNAKPNEVVSSLGSLSSNPSSLTTSKELSSASDGYIFN	360
BVH3-63	224	-----	223
BVH-3M	361	PKDIVEETATAYIVRHGDHFHYIPKSNQIGOPTLPNNSLATPSPSLPINPGTSHEKHEED	420
BVH3-63	224	-----TPSPSLPINPGTSHEKHEED	243

BVH-3M	421	GYGFDANRIIAEDES GFVMSHGDHNHYFFKKDLTEEQIKAAQKHLEEVKTS HNGLDLSS	480
BVH3-63	244	GYGFDANRIIAEDES GFVMSHGDHNHYFFKKDLTEEQIKAAQKHLEEVKTS HNGLDLSS	303

BVH-3M	481	HEQDYPGNAKEMKDLDDKKIEEKIAGIMQYGVKRESIVVNKEKNAI IYPHGDHHHADPID	540
BVH3-63	304	HEQDYPGNAKEMKDLDDKKIEEKIAGIMQYGVKRESIVVNKEKNAI IYPHGDHHHADPID	363

BVH-3M	541	EHKPVGIGHSHSNYELFKPEEGVAKKEGNKVYTGEELTNVNNLLKNSTFNNQNFTLANGQ	600
BVH3-63	364	EHKPVGIGHSHSNYELFKPEEGVAKKEGNKVYTGEELTNVNNLLKNSTFNNQNFTLANGQ	423

BVH-3M	601	KRVSFSPPELEKKLGINMLVKLITPDGKVLKESVSGKVFGEVGNIANFELDQPYLPGQT	660
BVH3-63	424	KRVSFSPPELEKKLGINMLVKLITPDGKVLKESVSGKVFGEVGNIANFELDQPYLPGQT	483

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*****
BVH-3M   661  FKYTEIASKDYPEVSYDGTFTVPTSLAYKMASQTIFYPPFHAGDTYLRVNPQFAVPKGTDAL  720
BVH3-63  484  FKYTEIASKDYPEVSYDGTFTVPTSLAYKMASQTIFYPPFHAGDTYLRVNPQFAVPKGTDAL  543
*****

BVH-3M   721  VRVFDEFHGNAYLENNYKVGEIKLPIPKLNQGTTRTAGNKIPVTFMANAYLDNQSTYIVE  780
BVH3-63  544  VRVFDEFHGNAYLENNYKVGEIKLPIPKLNQGTTRTAGNKIPVTFMANAYLDNQSTYIVE  603
*****

BVH-3M   781  VPILEKENQTDKPSILPQFKRNKAQENSKLDEKVEEPTSEKVEKEKLSETGNSTSNSTL  840
BVH3-63  604  VPILEKENQTDKPSILPQFKRNKAQENSKLDEKVEEPTSEKVEKEKLSETGNSTSNSTL  663
*****

BVH-3M   841  EEVPTVDPVQEKVAKFAESYGMKLENVLFNMDGTIELYLPSEGEVIKKNMADFTGEAPQGN  900
BVH3-63  664  EEVPTVDPVQEKVAKFAESYGMKLENVLFNMDGTIELYLPSEGEVIKKNMADFTGEAPQGN  723
*****

BVH-3M   901  GENKPSENGKVSTGTVENQPTENKPADSLPEAPNEKPVKPENSTDNGMLNPEGNVGSDPM  960
BVH3-63  724  GENKPSENGKVSTGTVENQPTENKPADSLPEAPNEKPVKPENSTDNGMLNPEGNVGSDPM  783
*****

BVH-3M   961  LDPAL EEAPAVDPVQEKLEKFTASYGLGLDSVIFNMDGTIELRLPSGEVIKKNLSDFIA  1019
BVH3-63  784  LDSAL EEAPAVDPVQEKLEKFTASYGLGLDSVIFNMDGTIELRLPSGEVIKKNLLIS  840
** *****

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FIGURE 31

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BVH-3      1  MKFSKKYIAAGSAVIVSLSLCAYALNQHRSEQENK-DNNRVSYVDGSQSSQKSENLTDPQV  59
BVH-11     1  MKINKKYL AG-SVATLVLSVCAYELGLHQAQTVK-ENNRVSYIDGKQATQKTENLTPDEV  58
BVH-11-2   1  MKINKKYL AG-SVAVLALSVCSYELGRHQAGQVKKESNRVSYIDGDQAGQKAENLTPDEV  59
          **  ***.* * . **.* * * . * . * . *****.* * . *****.*

BVH-3      60  SQKEGIQAEQIVIKITDQGYVTSBGDHYHYNGKVPYDALFSEELLMKDPNYQLKDADIV  119
BVH-11     59  SKREGINAEQIVIKITDQGYVTSBGDHYHYNGKVPYDAIISEELLMKDPNYQLKDS DIV  118
BVH-11-2   60  SKREGINAEQIVIKITDQGYVTSBGDHYHYNGKVPYDAIISEELLMKDPNYQLKDS DIV  119
          * . ***.*****.*****.*****.*****.***

BVH-3      120  NEVKG GYIIKVDGKYVYVLKDAAHADNVRTKDEINRQKQEHVKDNE----KVNSNVAVAR  175
BVH-11     119  NEIKGGYVIKVN GKYVYVLKDAAHADNVRTKEEINRQKQEHSHREGGTSANDGAVAFAR  178
BVH-11-2   120  NEIKGGYVIKVDGKYVYVLKDAAHADNIRTKEEIKRQKQEHSHNHN---SRADNAVAAR  176
          ** .***.* * . *****.* * . * . ***** * . * . * .

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SUBSTITUTE SHEET (RULE 26)

BVH-3	700	TVPTSLAYKMASQTIFYPFHAGDTYLRVNPQFAVPKGTDALVRVFDEFHGNAYLENNYKV	759
BVH-11	654	IIP---HYDHYHNIKFEWFDEG-----LYEAPKG-----YTLEDLLAT	688
BVH-11-2	640	IIP---HYDHYHNIKFEWFDEG-----LYEAPKG-----YSLEDLLAT	674
		. * . * . * * . * * . * *	
BVH-3	760	GEIKLPIPKLNQGTTRTAGNKIPVTFMANAYLDNQSTYIVEVPILEKENQTDKPSILPQF	819
BVH-11	689	VKYYVEHPNERPHSDNGFGN-----ASDHVQRN-----KNGQADTN-----	724
BVH-11-2	675	VKYYVEHPNERPHSDNGFGN-----ASDHVRKN-----KADQDSKP-----	710
		. * . * * . * . * *	
BVH-3	820	KRNKAQENSKLDEKVEEPTSEKVEKEKLSETGNSTSNSTLEEVPPTVDPVQEKVAKFAES	879
BVH-11	725	-----QTEKPSEEKQTEKPE---EE-----	742
BVH-11-2	711	-----DEDKEHDEVSEPTHPESDEKE-----	731
		* . . * *	
BVH-3	880	YGMKLENVLFNMDGTIELYLPSEGEVIKKNMADFTGEAPQGNGENKPSSENGKVSTGTVENQ	939
BVH-11	743	-----TPREEKPQSE---KPES-----PK	758
BVH-11-2	732	-----NHAGLNPSADNLYKPSTD-----TE	751
		* * *	
BVH-3	940	PTENKPADSLPEAPNEKPVKPENSTDNMGLNPEGNVGSDPMLDPALEEAPAVDPVQEKLE	999
BVH-11	759	PTEEPPEESPEES---EEPQVETEKVEEKLREAEDLLGK---IQDPIIKSN-----AKETLT	809
BVH-11-2	752	ETEEEAEDTTDEA---EIPQVENSVINAKIADAEALLEK---VTDPSIRQN-----AMETLT	802
		** . . * . * * . * . * * . * *	
BVH-3	1000	KFTASYGLGLDSVIFNMDGTIELRLPSGEVIKKNLSDFIA	1039
BVH-11	810	GLKNNLLFGTQ-----DNNTIMAEAEKLLALLKESK	840
BVH-11-2	803	GLKSSLLLGTK-----DNNTISAEVDSLLALLKESQPAPIQ	838
		* . * * . *	

FIGURE 32

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1  ATGCAAATTA CCTACACTGA TGATGAGATT CAGGTAGCCA AGTTGGCAGG CAAGTACACA
61 ACAGAAGACG GTTATATCTT TGATACTAGT TGGATTAAAA AAGATAGTTT GTCTGAAGCT
121 GAGAGAGCGG CAGCCCAGGC TTATGCTAAA GAGAAAGGTT TGACCCCTCC TTCGACAGAC
181 CACCAGGATT CAGGAAATAC TGAGGCAAAA GGAGCAGAAG CTATCTACAA CCGCGTGAAA
241 GCAGCTAAGA AGGTGCCACT TGATCGTATG CCTTACAATC TTCAGTATAC TGTAGAAGTC
301 AAAAACGGTA GTTTAATCAT ACCTCATTAT GACCATTACC ATAACATCAA ATTTGAGTGG
361 TTTGACGAAG GCCTTTATGA GGCACCTAAG GGGTATAGTC TTGAGGATCT TTTGGCGACT
421 GTCAAGTACT ATGTCGAACC GCGGAACGCT AGTGACCATG TTCGTAAAAA TAAGGCAGAC
481 CAAGATAGTA AACCTGATGA AGATAAGGAA CATGATGAAG TAAGTGAGCC AACTCACCTT
541 GAATCTGATG AAAAAGAGAA TCACGCTGGT TTAAATCCTT CAGCAGATAA TCTTTATAAA
601 CCAAGCACTG ATACGGAAGA GACAGAGGAA GAAGCTGAAG ATACCACAGA TGAGGCTGAA
661 ATTCTTGGTA CCCCTAGTAT TAGACAAAAT GCTATGGAGA CATTGACTGG TCTAAAAAGT
721 AGTCTTCTTC TCGGAACGAA AGATAATAAC ACTATTTCAG CAGAAGTAGA TAGTCTCTTG
781 GCTTTGTTAA AAGAAAGTCA ACCGGCTCCT ATACAGTAG (SEQ ID NO: 257)

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FIGURE 33

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1  MQITYTDDEI QVAKLAGKYT TEDGYIFDTS WIKKDSLSEA ERAAAQAYAK EKGLTPPSTD
61 HQDSCNTEAK GAEAIYNRVK AAKKVPLDRM PYNLQYTFEV KNGLIIPHY DHYHNKIFEW
121 FDEGLYEAPK GYSLEDLLAT VKYYVEPRNA SDHVRKNKAD QDSKPDEDKE HDEVSEPTHP
181 ESDEKENHAG LNPSADNLYK PSTDTEETEE EAEDTTDEAE IPGTPSIRQN AMETLTGLKS
241 SLLLGTKDNN TISAEVDSL L ALLKESQFAP IQ (SEQ ID NO : 258)

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FIGURE 34